

THOGERSEN=1

U.S. APPLICATION NO. (If known, see 37 CFR 1.5)

09/445576

INTERNATIONAL APPLICATION NO.  
PCT/DK98/00245INTERNATIONAL FILING DATE  
11 June 1998PRIORITY DATE CLAIMED  
11 June 1997TITLE OF INVENTION  
TRIMERISING MODULEAPPLICANT(S) FOR DO/EO/US  
Hans C. THOGERSEN et al.

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
  - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
  - b. ☒ has been transmitted by the International Bureau.
  - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
  - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
  - b. ☐ have been transmitted by the International Bureau.
  - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
  - d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☐ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☒ A FIRST preliminary amendment.  
☐ A SECOND or SUBSEQUENT preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information:
  1. A courtesy copy of the specification as originally filed.
  2. A courtesy copy of the first page of the International Publication (WO98/56906).
  3. A courtesy copy of the International Search Report.
  4. A courtesy copy of the International Preliminary Examination Report with annexes.  
Note: Please use the claims as they appear in the IPER annexes as the claims for examination in this case.
  5. Please note that the filing fee with respect to the claims is calculated based on the application as originally filed (including the amendments included on the Preliminary Amendment) and the additional claims fees due for the Supplemental Preliminary Amendment attached hereto.
  6. Formal drawings, 21 sheets, figures 1-21.

17. ☒ The following fees are submitted:**BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)) :**

Neither international preliminary examination fee (37 CFR 1.482)  
nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO  
and International Search Report not prepared by the EPO or JPO ..... \$970.00

International preliminary examination fee (37 CFR 1.482) not paid to  
USPTO but International Search Report prepared by the EPO or JPO ..... \$840.00

International preliminary examination fee (37 CFR 1.482) not paid to USPTO but  
international search fee (37 CFR 1.445(a)(2)) paid to USPTO ..... \$760.00

International preliminary examination fee paid to USPTO (37 CFR 1.482)  
but all claims did not satisfy provisions of PCT Article 33(1)-(4) ..... \$670.00

International preliminary examination fee paid to USPTO (37 CFR 1.482)  
and all claims satisfied provisions of PCT Article 33(1)-(4) ..... \$96.00

**ENTER APPROPRIATE BASIC FEE AMOUNT =**

CALCULATIONS PTO USE ONLY

\$ 840.00

Surcharge of \$130.00 for furnishing the oath or declaration later than ☐ 20 ☒ 30  
months from the earliest claimed priority date (37 CFR 1.492(e)).

\$ 130.00

| CLAIMS                                      | NUMBER FILED | NUMBER EXTRA | RATE       |           |  |
|---|--------------|--------------|------------|-----------|--|
| Total claims                                | 56 - 20 =    | 36           | X \$18.00  | \$ 648.00 |  |
| Independent claims                          | 1 - 3 =      |              | X \$78.00  | \$        |  |
| MULTIPLE DEPENDENT CLAIM(S) (if applicable) |              |              | + \$260.00 | \$        |  |

**TOTAL OF ABOVE CALCULATIONS =**

\$ 1,618.00

Reduction of 1/2 for filing by small entity, if applicable. A Small Entity Statement  
must also be filed (Note 37 CFR 1.9, 1.27, 1.28).

\$

**SUBTOTAL =**

\$ 1,618.00

Processing fee of \$130.00 for furnishing the English translation later than ☐ 20 ☐ 30  
months from the earliest claimed priority date (37 CFR 1.492(f)).

\$

**TOTAL NATIONAL FEE =**

\$ 1,618.00

Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be  
accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property

\$

**TOTAL FEES ENCLOSED =**

\$ 1,618.00

Amount to be:

refunded

\$

charged

\$

a. ☒ A check in the amount of \$ 1,618.00 to cover the above fees is enclosed.

b. ☐ Please charge my Deposit Account No. \_\_\_\_\_ in the amount of \$ \_\_\_\_\_ to cover the above fees.  
A duplicate copy of this sheet is enclosed.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any  
overpayment to Deposit Account No. 02-4035. A duplicate copy of this sheet is enclosed.

**NOTE:** Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

**BROWDY AND NEIMARK, P.L.L.C.****624 Ninth Street N.W., Suite 300****Washington, D.C. 20001**

SIGNATURE:

**Iver P. Cooper**

NAME

**28,005**

REGISTRATION NUMBER

**Date of this submission: December 13, 1999**



Applicant or Patented Henning Christian THØGERSEN et al. Attorney's  
Serial or Patent No.: US National stage of PCT/DK98/ Docket No.: THØGERSEN=1  
Filed or Issued: 13 December 1999 00245  
For: TRIMERISING MODULE

VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY  
STATUS (37 CFR 1.9(f) and 1.27(b) - INDEPENDENT INVENTOR

As a below named inventor, I hereby declare that I qualify as an independent inventor as defined in 37 CFR 1.9(c) for purposes of paying reduced fees under section 41(a) and (b) of Title 35, United States Code, to the Patent and Trademark Office with regard to the invention entitled TRIMERISING MODULE

described in

- ☐ the specification filed herewith  
☒ application serial no. \_\_\_\_\_, filed 13 December 1999  
☐ patent no. \_\_\_\_\_, issued \_\_\_\_\_

I have not assigned, granted, conveyed or licensed and am under no obligation under contract or law to assign, grant, convey or license, any rights in the invention to any person who could not be classified as an independent inventor under 37 CFR 1.9(c) if that person had made the invention, or to any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e).

Each person, concern or organization to which I have assigned, granted, conveyed, or licensed or am under an obligation under contract or law to assign, grant, convey, or license any rights in the invention is listed below:

- ☐ no such person, concern, or organization  
☒ persons, concerns or organizations listed below\*

\*Note: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

NAME Protein Engineering Technology ApS  
ADDRESS Gustav Wieds Vej 10, DK-8000 Århus C, Denmark  
☐ INDIVIDUAL ☒ SMALL BUSINESS CONCERN ☐ NONPROFIT ORGANIZATION

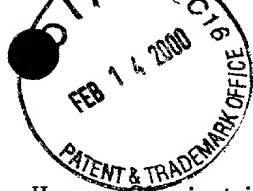
NAME \_\_\_\_\_  
ADDRESS \_\_\_\_\_  
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I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b))

I hereby declare that all statements made herein of my own knowledge are true and that all statements on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

Ingrid Kjøller LARSEN

| NAME OF INVENTOR      | NAME OF INVENTOR      | NAME OF INVENTOR      |
|-----------------------|-----------------------|-----------------------|
| <u>Ingrid Kjøller</u> |                       |                       |
| Signature of Inventor | Signature of Inventor | Signature of Inventor |
| <u>19-1-2000</u>      |                       |                       |
| Date                  | Date                  | Date                  |



Applicant or Patentee: Hans Christian THØGERSEN et al. Attorney's  
Serial or Patent No.: US National stage of PCT/DK98/ Docket No.: THØGERSEN=1  
Filed or Issued: 13 December 1999 00245  
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Bettina Bryde NIELSEN

| NAME OF INVENTOR       | NAME OF INVENTOR      | NAME OF INVENTOR      |
|------------------------|-----------------------|-----------------------|
| <i>Bettina Nielsen</i> |                       |                       |
| Signature of Inventor  | Signature of Inventor | Signature of Inventor |
| <u>19-1-2000</u>       |                       |                       |
| Date                   | Date                  | Date                  |





Applicant or Patentee: Hans Christian THØGERSEN et al. Attorney's  
Serial or Patent No.: US National stage of PCT/DK98/ Docket No.: THØGERSEN=1  
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Jette Sandholm KASTRUP

NAME OF INVENTOR

NAME OF INVENTOR

NAME OF INVENTOR

Signature of Inventor

Signature of Inventor

Signature of Inventor

Date

Date

Date



Applicant or Patentee: Hans Christian THØGERSEN et al. Attorney's  
Serial or Patent No.: US National stage of PCT/DK98/ Docket No.: THØGERSEN=1  
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|   |                       |                       |
|---|-----------------------|-----------------------|
| <u>Hans Christian THØGERSEN</u>   |                       |                       |
| NAME OF INVENTOR  | NAME OF INVENTOR      | NAME OF INVENTOR      |
|  |                       |                       |
| Signature of Inventor   | Signature of Inventor | Signature of Inventor |
| <u>17. januar 2000</u>  |                       |                       |
| Date  | Date                  | Date                  |



Applicant or Patentee: Hans Christian THØGERSEN et al. Attorney's  
Serial or Patent No.: US National stage of PCT/DK98/ Docket No.: THØGERSEN=1  
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Niels Jonas Heilskov GRAVERSEN

NAME OF INVENTOR NAME OF INVENTOR NAME OF INVENTOR

Signature of Inventor Signature of Inventor Signature of Inventor

Date Date Date



Applicant or Patentee: Hans Christian THØGERSEN et al. Attorney's  
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Thor Las HOLTET  
NAME OF INVENTOR NAME OF INVENTOR NAME OF INVENTOR  
Thor Las Holtet  
Signature of Inventor Signature of Inventor Signature of Inventor  
01.25.2000  
Date Date Date



Applicant or Patentee: Hans Christ~~ian~~ THOGERSEN et al. Attorney's  
Serial or Patent No.: US National stage of PCT/DK98/ Docket No.: THOGERSEN=1  
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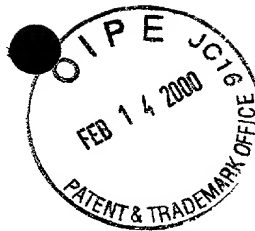
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Michael ETZERODT

| NAME OF INVENTOR        | NAME OF INVENTOR      | NAME OF INVENTOR      |
|-------------------------|-----------------------|-----------------------|
| <u>Michael Etzerodt</u> |                       |                       |
| Signature of Inventor   | Signature of Inventor | Signature of Inventor |
| <u>01.12.2000</u>       |                       |                       |
| Date                    | Date                  | Date                  |



PATENT

APPLICANT OR PATENTEE: Hans Christian Thøgersen et al. Docket  
SERIAL OR PATENT NO.: US National stage of PCT/DK98/ No. THOGERSEN = 1  
FILED OR ISSUED: 13 December 1999 00245  
FOR: TRIMERISING MODULE

**VERIFIED STATEMENT (DECLARATION) CLAIMING  
SMALL ENTITY STATUS (37 CFR 1.9(f) and  
1.27(c)) -- SMALL BUSINESS CONCERN**

I hereby declare that I am:

☐ the owner of the small business concern identified below.

☒ an official of the small business concern empowered to act on  
behalf of the concern identified below.

NAME OF CONCERN: Protein Engineering Technology ApS  
ADDRESS OF CONCERN: Gustav Wieds Vej 10, DK-8000 Århus C, Denmark

I hereby declare that the above identified small business concern qualifies as a small business concern as defined in 13 CFR 121.3-18, and reproduced in 37 CFR 1.9(d), for purposes of paying reduced fees under Section 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention, entitled

TRIMERISING MODULE

by inventor(s) H. C. Thøgersen, M. Etzerodt, T. L. Holtet,  
N. J. H. Graversen, J. Kastrup, B.B. Nielsen, and I. K. Larsen  
described in

☐ the specification filed herewith

☒ application serial no. \_\_\_\_\_, filed 13 December 1999

☐ patent no. \_\_\_\_\_, issued \_\_\_\_\_

If the rights held by the above-identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below\* and no rights to the invention are held by any person, other than the inventor, who would not qualify as

a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e). NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

NAME: \_\_\_\_\_

ADDRESS: \_\_\_\_\_

☐ Individual ☐ Small Business Concern  
☐ Nonprofit Organization

NAME: \_\_\_\_\_

ADDRESS: \_\_\_\_\_

☐ Individual ☐ Small Business Concern  
☐ Nonprofit Organization

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b))

I hereby declare that all statements made herein are of my own knowledge, are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING: Jens Lübeck JOHANSEN

TITLE OF PERSON OTHER THAN OWNER: Chairman of the Board of Directors

ADDRESS OF PERSON SIGNING: \_\_\_\_\_

SIGNATURE

Jens Lübeck JOHANSEN

DATE

2/1 2000

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

|                         |   |                         |
|-------------------------|---|-------------------------|
| In re Application of:   | ) | Art;Unit:               |
| Hans THOGERSEN et al.   | ) |                         |
| IA No.: PCT/DK98/00245  | ) |                         |
| IA Filed: 11 June 1998  | ) | Washington, D.C.        |
| U.S. App. No.:          | ) |                         |
| (Not Yet Assigned)      | ) |                         |
| National Filing Date:   | ) | December 13, 1999       |
| (Not Yet Received)      | ) |                         |
| For: TRIMERISING MODULE | ) | Docket No.: THOGERSEN=1 |

PRELIMINARY AMENDMENT

Honorable Commissioner of Patents and Trademarks  
Washington, D.C. 20231

Sir:

Contemporaneous with the filing of this case and  
prior to calculation of the filing fee, kindly amend as  
follows:

IN THE SPECIFICATION

After the title please insert the following  
paragraph:

--CROSS REFERENCE TO RELATED APPLICATION

The present application is the national stage under  
35 U.S.C. 371 of PCT/DK98/00245, filed June 11, 1998. --

IN THE CLAIMS

Please amend the claims as follows:

-- 1 (amended). A monomer polypeptide construct  
comprising at least one tetranectin trimerising structural  
element (TTSE) which is covalently linked to at least one  
heterologous moiety, said TTSE being capable of forming a



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stable triple alpha helical coiled coil complex with two other TTSEs, [with the proviso that] where (a) the heterologous moiety is different from any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12M H6FCTN23, the sequences of which are shown in SEQ ID NOs:24-27[.]; and/or (b) at least one heterologous moiety being one in which does not exclusively facilitate expression and/or purification of the monomer polypeptide construct.

2 (amended). [A] The monomer polypeptide construct [comprising at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, said TTSE being capable of forming a stable triple alpha helical coiled coil complex with two other TTSEs, said at least one heterologous moiety being one which does not exclusively facilitate expression and/or purification of the monomer polypeptide construct] of claim 1 where (a) applies. --

Claim 3, line 1, replace "A" with --The--; and  
line 1, replace "any of the preceding claims"  
with --claim 1--.

Claim 4, line 1, replace "A" with --The--; and  
line 1, replace "any of the preceding claims"  
with --claim 1--.

Claim 5, line 1, replace "A" with --The--.

Claim 6, line 1, replace "A" with --The--; and  
line 1, delete "or 5".

Claim 7, line 1, replace "A" with --The--; and  
line 1, replace "any of claims 1-3" with

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--claim 1--.

Claim 8, line 1, replace "A" with --The--; and  
line 1, replace "any of the preceding claims"  
with --claim 1--.

Claim 9, line 1, replace "A" with --The--.

Claim 10, line 1, replace "A" with --The--; and  
line 2, delete "such as at least 81% at least  
87%, or at least 92%".

Claim 11, line 1, replace "A" with --The--; and  
line 1, replace "any of claims 8-10" with  
--claim 8--.

Claim 12, line 1, replace "A" with --The--; and  
line 1, replace "any of the preceding claims"  
with --claim 1--.

Claim 13, line 1, replace "A" with --The--.

Claim 14, line 1, replace "A" with --The--; and  
line 1, replace "any of the preceding claims"  
with --claim 1--.

Claim 15, line 1, replace "A" with --The--; and  
line 1, replace "any of the preceding claims"  
with --claim 1--.

Claim 16, line 1, replace "A" with --The--; and  
line 1, replace "any of the preceding claims"  
with --claim 1--.

Claim 17, line 1, replace "A" with --The--; and

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line 1, replace "any of the preceding claims" with --claim 1--.

Claim 18, line 1, replace "A" with --The--; and

line 1, replace "any of the preceding claims" with --claim 1--.

-- 19 (amended). An oligomer [which is comprised of] comprising at least two monomer polypeptide constructs according to [any of claims 1-18 and which comprises at least three TTSE's or a multiplum of three TTSE's, or which is comprised of three monomer polypeptide constructs according to any of claims 1-3 or 7-18] claim 1. --

Claim 21, line 1, delete "or 20".

Claim 24, line 1, replace "any of claims 19-23" with --claim 19--.

Claim 25, line 1, replace "any of claims 1-18" with --claim 1--.

Claim 26, line 1, delete "according to claim 19";

line 2, replace "any of claims 1-18" with --claim 1--; and

lines 3 and 4, replace "any of claims 1-3 or 7-18" with --claim 1--.

Claim 27, line 1, delete "according to claim 19"; and

line 2, replace "any of claims 1-18" with --claim 1--.

Claim 28, line 3, replace "any of claims 1-18" with --claim 1--;

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lines 5 and 6, replace "any of claims 1-18"  
with --claim 1--; and

lines 9 and 10, replace "any of claims 1-3 or  
7-18" with --claim 1--.

Claim 30, line 1, delete "or 29".

Claim 31, line 1, replace "any of claims 1-18" with  
--claim 1--; and

lines 2 and 3, replace "any of claims 1-18"  
with --claim 1--.

Delete claim 34 in its entirety.

Claim 35, line 1, replace "use" with --method--; and

line 1, replace "34" with --65--; and

line 1, replace "moity" with --moiety--.

-- 36 (amended). [The use of a monomer polypeptide  
construct according to any of claims 1-18 or to a an oligomer  
according to any of claims 9-24 as a] A component of a chimaeric  
product having low antigenicity in humans relative to formulations  
comprising one or more components of non-human origin, and  
comprising at least one monomer polypeptide construct according to  
claim 1.

37 (amended). [The use] In a method of [a monomer  
polypeptide construct according to any of claims 1-18 or to a an  
oligomer according to any of claims 19-24 as a vehicle for]  
assembling antibody fragments into oligometric or multivalent  
entities for generating chimeric artificial antibodies having  
preselected pharmacokinetic and/or pharodynamic properties the

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improvement which comprises use of at least one monomer polypeptide construct according to claim 1 as a vehicle.

38 (amended). The [use] method of claim 48 comprising [a monomer polypeptide construct according to any of claims 1-18 or to a an oligomer according to any of claims 19-24 for] delivering an imaging or toxin-conjugated antibody to a tumor.

39 (amended). [The use of a monomer polypeptide construct according to any of claims 1-18 or to a oligomer according to any of claims 19-24 as a vehicle delivering an] In a method of delivering a substance to a target cell or tissue, the improvement which comprises use of a conjugate of said substance and at least one monomeric polypeptide construct according to claim 1. --

Delete claims 40-46 in their entirety.

-- 47 (amended). [The use according to any of claims 34 to 46 wherein the] A composition comprising at least one monomer polypeptide construct according to claim 1 [any of claims 1-18 or the oligomer according to any of claims 19-21 is comprised] in a liposome.

48 (amended). A method for treating or preventing a disease comprising administering to [the] a subject in need thereof a therapeutically or prophylactically effective amount of a [an effective amount of a pharmaceutical composition as defined in any of claims 44 and 45] pharmaceutically acceptable composition comprising

(a) a pharmaceutical comprising at least one monomer

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polypeptide construct according to claim 1, or

(b) a gene therapy vector comprising DNA encoding a pharmaceutical of (a) above. --

Delete claims 49 and 50 in their entirety.

Claim 51, lines 1 and 2, replace "A method of human gene therapy comprising use of a monomer polypeptide construct according to any of claims 1-18 or to an oligomer according to any of claims 19-24" with --The method of claim 65--.

Claim 52, line 1, replace "A" with --The--;

line 1, replace "any of claims 48 to 51"

with

--claim 48--;

lines 2 and 3, replace "monomer polypeptide construct according to any of claims 1-18 or the oligomer according to any of claims 19-24" with --composition--; and

line 6, delete "such as a tumour".

Delete claim 53 in its entirety.

-- 54 (amended). A method for diagnosis of a disease comprising a [construct comprising the monomer polypeptide construct according to any of claims 1-18 or the oligomer according to any of claims 19-24 together with a diagnosing component coupled thereon] contacting a sample with a diagnostic agent according to claim 66, and correlating the degree of interaction between the agent and the sample, with the status of the disease. --

Please add the following claims:

-- 55. The monomer polypeptide construct of claim 1

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where (b) applies.

56. The monomer polypeptide construct of claim 2 where (b) applies.

57. The monomer polypeptide construct of claim 1 which comprises a plurality of TTSEs.

58. The monomer polypeptide construct of claim 1 which comprises at least three TTSEs.

59. The monomer polypeptide construct of claim 1 which has exactly an integer ( $\geq 1$ ) multiple of three TTSEs.

60. The oligomer of claim 24, comprising at least three monomer polypeptide constructs.

61. An oligomer comprising at least two monomer polypeptide constructs according to claim 59.

62. The method of claim 48 in which the pharmaceutical is a monomer polypeptide construct.

63. The method of claim 48 in which the pharmaceutical is an oligomer comprising at least two monomer polypeptide constructs.

64. The method of claim 48 in which (a) is administered.

65. The method of claim 48 in which (b) is administered.

66. A diagnostic agent comprising at least one monomer polypeptide construct according to claim 1, and a detectable label or an insoluble support.

67. In a method of displaying a protein library the

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improvement which comprises operably linking the library proteins to a living or nonliving support by means of at least one monomer polypeptide construct according to claim 1. --

If, inadvertently, a proper multiple dependent claim has not been amended to reduce it to single dependency, please amend it to be dependent solely on the first-mentioned claim, or, if that is not possible, please cancel the claim and notify the undersigned.

REMARKS

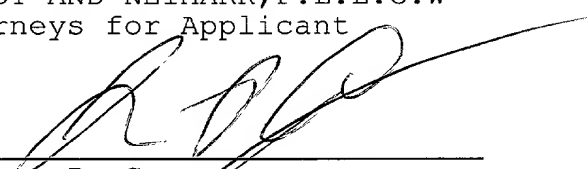
The above amendment to the specification is being made to insert reference to the PCT application of which the present case is a U.S. national stage. The above amendments to the claims are being made in order to eliminate any properly multiply dependent claims, for the purpose of reducing the filing fee and to place the claims into better form for examination in the U.S. Please enter this amendment prior to calculation of the filing fee in this case.

Favorable consideration and allowance are earnestly solicited.

Respectfully submitted,

BROWDY AND NEIMARK, P.L.L.C.w  
Attorneys for Applicant

By

  
Iver P. Cooper  
Registration No. 28,005

IPC:bcs  
Telephone No.: (202) 628-5197  
Facsimile No.: (202) 737-3528  
f:\filing\preliminary amendments\thogersen1.wpd



PTO/PCT Rec'd 13 DEC 1999

TRIMERISING MODULE

The present invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family, and their use in rational *de novo* design and production of multi-functional molecules including the application of the multi-functional molecules in protein library technology, such as phage display technology, diagnostic and therapeutic systems, such as human gene therapy and imaging.

## 10 BACKGROUND OF THE INVENTION

Tetranectin is a  $\text{Ca}^{2+}$ -binding trimeric C-type lectin which is present in blood plasma and from the extracellular matrix of certain tissues. The tetranectin group of proteins comprises tetranectin isolated from man and from mouse and the highly related C-type lectin homologues isolated from the cartilage of cattle (Neame and Boynton, database accession number PATCHX:u22298) and from reef shark (Neame et al., 1992, Neame et al., 1996 and database accession number p26258 and PIR2:A37289).

20 The mature tetranectin polypeptide chain of 181 amino acid residues is encoded in three exons as shown by molecular cloning and characterisation of the gene (Berglund & Petersen, 1992; Wewer & Albrechtsen, 1992). Exon 3 of the human tetranectin gene encodes a separate functional and structural unit, a single long-form so-called carbohydrate recognition domain (CRD), with three intra-chain disulphide bridges. The tetranectin CRD is considered to belong to a distinct class of C-type lectins (Day, 1994) clearly related to C-type lectins by sequence homology, conservation of disulphide topology (Fuhlendorff et al., 1987) and by the presence of an almost conserved suit of amino acid residues known to be involved in binding of calcium ions.

A published poster (Holtet et al 1996) has proposed tetranectin to be a trimer and that trimerisation is governed by the peptide encoded by exon 1. The peptide encoded by exon 1 was proposed to be "necessary and sufficient to govern trimerisation" whereas the polypeptide encoded by exon 2 was proposed as being "involved in lysine-sensitive binding to plasminogen".

Tetranectin was first identified as a plasma protein binding to plasminogen by binding to the kringle-4 domain of plasminogen. Recent unpublished results (Graversen et al., manuscript for PNAS) proves (1) that the site in tetranectin involved in binding to plasminogen resides entirely in the CRD-domain (encoded by exon 3), (2) that binding is calcium sensitive, and (3) that the kringle-4 binding site in tetranectin overlaps the putative carbohydrate binding site of the CRD domain. Hence, there is now surprising definitive evidence that TN exons 1 and 2, i.e. the trimerisation unit in TN does not exhibit any plasminogen-binding affinity. Accordingly, an artificial protein containing a TTSE unit as part of its architecture is not expected to interact with plasminogen or plasmin due to properties inherited from tetranectin.

Tetranectin has also been reported to bind to sulfated polysaccharides like heparin (Clemmensen (1989) Scand J. Clin. Lab. Invest. vol 49:719-725). We have new results showing that the CRD domains of tetranectin are not involved in this protein-polysaccharide interaction. In fact, the site in tetranectin is located in the N-terminal region of exon 1 and may be abolished by removal or mutagenesis of N-terminal lysine residues (Graversen et al., manuscript), processes that do not inhibit trimerisation. TTSEs that include most or all of TN exon 1 therefore confer an affinity for sulfated polysaccharides to any designed protein which encompasses such a TTSE as part of its structure. If desired, however, this affinity can be reduced or abolished by N-terminal truncation or mutagenesis of lysine residues in the part of

the TTSE that corresponds to the N-terminal 8-10 amino acid residues of exon 1 (Graversen et al., unpublished).

With respect to gene therapy which is also within the scope of the present invention, there is only a limited number of basic strategies for gene therapy which show some promise in preclinical models so far. The two major strategies e.g. for the treatment of malignant tumors are cytokine-gene aided tumor vaccination and selective prodrug activation. Whereas the first strategy relies on the strong immunostimulatory effect of a relatively small number of genetically modified cytotoxic T cells or tumor cells, the second one is based on conversion of a nontoxic prodrug into a toxic product by an enzyme-encoding gene where the toxic effect is exerted also on non-transduced dividing tumor cells due to a so-called bystander effect. Alternatively, strategies can be envisaged where the malignant phenotype of a cell is reversed by either inactivating an oncogene or reestablishing an inactivated tumor suppressor gene. In both cases, highly efficient gene transfer to the cells in a tumor is required. Although high efficiencies of gene transfer can be obtained *in vitro* and even *in vivo* under certain circumstances, correction of the malignant phenotype by reversing the major oncogenic change in the tumor cells is unlikely to result in normal cells. Thus, selective induction of tumor cell death by use of the present invention would be preferable, and the development of methods enabling such induction will be of great importance.

A major problem in connection with the gene therapy is the incorporation of foreign material into the genome. Viruses, however, have only been partially successful in overcoming this problem. Hence the initial efforts at gene therapy are still directed towards engineering viruses so that they could be used as vectors to carry therapeutic genes into patients. In the still very immature *in vivo* method of somatic gene therapy, where a vector could be injected directly into the bloodstream, or more preferably by transmucosal delivery, the present invention may be utilized due to the surprising number of ways the gene therapy may be targeted.

For many gene-therapy applications in the future, it is probable that a synthetic hybrid system will be used that incorporates engineered viral component for target-specific binding and core entry, immunosuppressive genes from various  
5 viruses and some mechanism that allows site-specific integration, perhaps utilizing AAV sequences or an engineered retroviral integrase protein. In addition, regulatory sequences from the target cell itself will be utilized to allow physiological control of expression of the inserted  
10 genes. All these components would be assembled in vitro in a liposome-like formulation with additional measures taken to reduce immunogenicity such as concealment by PEG

As mentioned, one of the current problems in gene therapy is the efficient delivery of nucleic acids to as many as  
15 possible of a specific population of cells in the body, and it is often not possible to find e.g. an appropriate viral vector that will find that particular cell population efficiently and selectively (Review on aspects of gene therapy: Schaper, W & Ito, W.D. Current Opinion in  
20 Biotechnology, 1996, vol. 7, 635-640. Nature Biotechnology 1998 vol 16 is an entire volume dedicated to protein- and gene delivery).

Given the possibility of in vitro generation of a human antibody against virtually any target antigen by phage  
25 technology, it follows that TTSEs, where one of the subunits is modified with a membrane integrating or associating entity, may be used as a practicable tool for generating a viral, bacterial or preferentially artificially assembled lipomal vehicle that will allow selective delivery of the  
30 contained material by infection or transfection of any cell population to which such a specific antibody may be generated. Moreover vehicles may, with the use of TTSEs, be individualised by selection of patient specific antibodies or by assembling TTSE units conjugated with scFvs selected from  
35 an ensemble of antibodies selected by the particular markers of the disease.

## SUMMARY OF THE INVENTION

It has surprisingly been found by the present inventors that the human tetranectin polypeptide (and derivatives thereof) is capable of forming very stable trimers which have a number of advantageous characteristics and uses. Notably, the tetra-

5 nectin molecule includes a trimerising structural element which can be used as carrier of other chemical entities, thereby providing a carrier molecule of a hitherto unseen versatility.

10 Prior published knowledge in the field of providing trimerising polypeptides of choice includes the disclosure in WO 95/31540 by Hoppe and Reid which describes a trimerisation module derived from collectin coiled coil structures and its application in engineering of artificially trimerised pro-

15 teins. Several interesting areas of application are common to that patent publication and to the present disclosure. However, in several ways the properties of the trimerisation modules derived from the tetranectin protein family as disclosed herein are markedly different in fundamental architecture and represent surprisingly improved properties in comparison with the collectin trimerisation unit:

20

(1) Although the spatial structures of both trimerisation modules at a superficial level appear as similar in that both are ternary coiled coil structures of roughly equivalent

25 spatial size the structural basis for adopting this spatial configuration is markedly distinct between the two groups of proteins. In fact, it is so distinct that the common belief prior to the work of Holtet et al. on cross-linking of human tetranectin (Holtet et al., 1996) was that this family of

30 proteins were tetrameric (hence the name). Accordingly, the sequences of the tetranectin family of trimerisation modules does not conform to the declared common motif delineated for the collectin family (WO 95/31540, page 8).

(2) The thermal stability of the tetranectin trimerisation module (as shown in the examples) is such that the trimer can be shown to exist even at about 60°C (Example 4, trimerised tetranectin) or at about 70°C (Example 3, trimerised ubiquitin), whereas a collectin trimer unit falls apart at about 50-55°C (WO 95/31540, Example 1, page 36 therein).

(3) Whereas it remains uncertain whether the collectin trimerisation domain possibly allows attachment of fusion partners at C-terminal ends of the trimerisation module, and whereas no example has been reported of successful or claimed successful attachment of a foreign protein (except for the GST fusion partner) to the N-terminal region of the collectin trimerisation module, the information disclosed herein demonstrates that the tetranectin trimerisation module is more versatile in that it allows attachment of foreign proteins to either, as well as to both, terminus or termini simultaneously (Examples 1-4). This has important consequences as the tetranectin trimerisation module may be deployed to construct molecules that are able to interact (each end with a binding valency up to 3) simultaneously with two bulky interaction partners like e.g. cell surfaces.

(4) The virtual absence of subunit exchange between monomers of a trimer that has been trimerised using the tetranectin trimerisation modules disclosed herein is by first principles of thermodynamics correlated with the surprisingly high thermal stability of the complex. It will hence be apparent that the advantages inherent to the "pick-and-mix" applications of the technology, as disclosed herein, may be used to much greater advantage because of the much longer shelf life expected for the heterofunctional products of the present invention.

The polypeptide constructs CIIH6FXTN123, H6FXTN123, H6FXTN12, and H6FXTN23 which all involve parts of the tetranectin molecule have previously been prepared (cf. e.g. WO 94/18227) but these constructs have all been provided with a view to

facilitating expression and/or purification of the tetranectin derived moiety of the constructs. To the best of the inventors' knowledge no publications exist which reports any use of tetranectin derivatives as "building blocks" to which  
5 other chemical moieties advantageously could be coupled.

Hence, in its broadest aspect the present invention relates to a monomer polypeptide construct comprising at least one tetranectin trimerising structural element (hereinafter designated a TTSE) which is covalently linked to at least one  
10 heterologous moiety, said TTSE being capable of forming a stable complex with two other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23, the sequences of which are shown in SEQ ID NOs: 24-27. It is  
15 preferred that the heterologous moiety is one which does not exclusively facilitate expression and/or purification of the monomer polypeptide construct.

The invention further relates to oligomeric molecules comprised of at least two of such monomer polypeptide constructs, and the invention also relates to methods of preparing the monomer polypeptide constructs and the oligomers. The invention further relates to a kit comprising monomer polypeptide constructs in separate packages, ready for use in  
25 a "pick-and-mix" approach for use of the monomers. This pick and mix approach is for use in therapeutic as well as for diagnostic use. Eg. having a tumor with a known and specific epitope to which an antibody is available. The kit may then comprise a first TTSE conjugated to an relevant antibody, a  
30 second component which may comprise a TTSE coupled to an imaging compound. In a second aspect the second component may comprise a drug or a prodrug relevant for treating the tumor. In a still further aspect a third TTSE component being a monitoring compound, e.g. indicative of the progress of the  
35 targeting.

As is clear from this illustration the present invention relates to a large amount of combinations allowing an individual design for a large number of circumstances.

Finally, the invention also pertains to fragments which include nucleic acid sequences which encode the monomer polypeptide constructs, as well as to vectors and cells containing these nucleic acid fragments.

#### LEGENDS TO THE FIGURES

Fig. 1: Amino acid sequence of the amino terminal region of tetranectin.

Amino acid sequence (in one letter code) from E1 to L51 of tetranectin (SEQ ID NO: 7). Exon 1 comprises residues E1 to D16 and exon 2 residues V17 to V49, respectively. The alpha helix extends beyond L51 to K52 which is the C-terminal amino acid residue in the alpha helix.

Fig. 2: Alignment of the amino acid sequences of the trimerising structural element of the tetranectin protein family. Amino acid sequences (one letter code) corresponding to residue V17 to K52 comprising exon 2 and the first three residues of exon 3 of human tetranectin (SEQ ID NO: 7); murine tetranectin (Sørensen et al., Gene, 152: 243 -245, 1995); tetranectin homologous protein isolated from reef-shark cartilage (Neame and Boynton, 1992,1996); and tetranectin homologous protein isolated from bovine cartilage (Neame and Boynton, database accession number PATCHX:u22298). Residues at a and d positions in the heptad repeats are listed in boldface. The listed consensus sequence of the tetranectin protein family trimerising structural element comprise the residues present at a and d positions in the heptad repeats shown in the figure in addition to the other conserved residues of the region. "hy" denotes an aliphatic hydrophobic residue.



Fig. 3: Construction of the expression plasmids pTH6FXtripa and pTH6FXtripb.

The amplified DNA fragments tripa and tripb harbouring the tetranectin amino acid sequence (SEQ ID NO: 7) from E1 to T48 and E1 to K52, respectively, fused in the 5' end to nucleotide sequences encoding a FX<sub>a</sub> cleavage site IQGR (SEQ ID NO: 4) and the recognition sites for the restriction endonucleases BglIII and KpnI, were cut with the restriction enzymes BclI and HindIII and ligated into the BamHI and HindIII sites of the expression plasmid pT7H6 (Christensen et al., 1991) using standard procedures.

Fig. 4: Predicted amino acid sequence of the fusion proteins H6FXtripa (SEQ ID NO: 28) and H6FXtripb (SEQ ID NO: 29) encoded by the expression plasmids pTH6FXtripa and pTH6FXtripb, respectively.

Fig. 5: Construction of the expression plasmids pTH6FXTN123 and pTCIIH6FXTN123.

The amplified DNA fragment corresponding to the full length, mature tetranectin monomer (SEQ ID NO: 7) from E1 to V181 fused in the 5' end to nucleotide sequences encoding a FX<sub>a</sub> cleavage site IEGR (SEQ ID NO: 10) was cut with the restriction enzymes BamHI and HindIII and ligated into the corresponding sites of the expression plasmids pT7H6 (Christensen et al., 1991) and pTCIIH6 using standard procedures. pTCIIH6 was derived from pT7H6 by substitution of the NdeI - HindIII fragment of pT7H6 with the NdeI - HindIII fragment of pLcII (Nagai and Thøgersen, 1987) encoding the first 32 residues of the lambda cII protein MVRANKRNEALRIESALLNKIAMLGTEKTAEG (SEQ ID NO: 11) fused in the 3' end to a nucleotide sequence encoding the H6 sequence GSHHHHHHGS (SEQ ID NO: 12).

Fig. 6: Predicted amino acid sequence of the fusion proteins H6FXTN123 (SEQ ID NO: 25) and CIIH6FXTN123 (SEQ ID NO: 24) encoded by the expression plasmids pTH6FXTN123 and pTCIIH6FXTN123, respectively.

Fig. 7: Construction of the expression plasmids pTH6FXTN12, pTH6FXTN23, and pTH6FXTN3.

The amplified DNA fragments corresponding to the tetranectin derivatives TN12 and TN3 from E1 to V49 and A45 to V181, respectively (SEQ ID NO: 7) fused in the 5' end to nucleotide sequences encoding the FX<sub>a</sub> cleavage site IEGR (SEQ ID NO: 10) was cut with the restriction enzymes BamHI and HindIII and ligated into the corresponding sites of the expression plasmids pT7H6 (Christensen et al., 1991) using standard procedures. The amplified DNA fragment corresponding to the tetranectin derivative TN23 from V17 to V181 (SEQ ID NO: 7) fused in the 5' end to nucleotide sequences encoding the FX<sub>a</sub> cleavage site IQGR (SEQ ID NO: 4) was cut with the restriction enzymes BamHI and HindIII and ligated into the corresponding sites of the expression plasmids pT7H6 (Christensen et al., 1991) using standard procedures.

Fig. 8: Predicted amino acid sequence of the fusion proteins H6FXTN12 (SEQ ID NO: 26), H6FXTN23 (SEQ ID NO: 27), and H6FXTN3 (SEQ ID NO: 30) encoded by the expression plasmids pTH6FXTN12, pTH6FXTN23, respectively.

Fig. 9: Gel filtration analysis of TN123, TN23, and TN3. Analytical gel filtration of the recombinant tetranectin derivatives TN123, TN23, and TN3 were performed on a Superose 12 HR 10/30 column (Pharmacia, Sweden) with a total volume of 25 ml in 100 mM NaCl and 50 mM Tris-HCl pH 8 and a flow rate of 0.2 ml/min. Vertical bars at peak maxima identify elution profiles for each of the three proteins.

Fig. 10: Cross-linking analysis of TN123 and CIIH6FXTN123. Samples of TN123, CIIH6FXTN123 and mixtures of both were incubated with DMSI and analyzed by SDS-PAGE (12% gel). Before addition of DMSI, protein mixtures were subjected to subunit exchange by incubation at 70°C for varying length of time. Protein marker of 94, 68, 43 and 30 kDa, top to bottom (lane M). CIIH6FXTN123 fusion protein (lane 1). TN123 (lane 2). DMSI treated CIIH6FXTN123 (lanes 3 and 6). DMSI-treated

TN123 (lane 4). Identical samples of DMSI treated mixtures of CIIH6FXTN123 and TN123 without heat exposure (lanes 5 and 7) and heat treated for 2.5 sec, 15 sec, 2.5 min. and 10 min., respectively, before treatment with DMSI (lanes 8-11).

- 5 Fig. 11: Cross-linking analysis of the recombinant tetranectin derivatives TN123, TN23, TN3, and H6FXTN12.  
The recombinant proteins TN123, TN23, TN3, H6FXTN12 or mix-  
tures of TN123 and each of the other were analyzed by SDS-  
PAGE. Protein marker of 94, 68, 43, 30, 20, and 14.4 kDa, top  
10 to bottom (lane M). TN123 cross-linked with DMSI (lane 1).  
TN123 and H6-rTN12 cross-linked with DMSI without and with  
heat treatment at 70°C for two min. (lanes 2 and 3). H6FXTN12  
cross-linked with DMSI (lanes 4 and 5). Mixture of TN123 and  
H6FXTN12, no cross-linking (lane 6). Cross-linking of TN123  
15 and TN23 without and with heat treatment at 70°C for two min.  
(lanes 7 and 8). Cross-linking of TN23 (lane 9). Mixture of  
TN123 and TN23 without cross-linking (lane 10). TN123 cross-  
linked by DMSI (lane 11). Cross-linking of TN123 and TN3  
without and with heat treatment for two min. (lanes 12 and  
20 13). Cross-linking of TN3 (Lane 14). Mixture of TN123 and  
TN3, no cross-linking (lane 15).

Fig. 12: Cross-linking based analysis of the trimer thermal stability.

- In parallel experiments TN123 and the fusion protein  
25 H6FXtripb-UB (SEQ ID NO: 31) were cross-linked with DMSI at  
different temperatures and the samples analyzed by SDS-PAGE.  
Protein marker of 94, 68, 43, 30, 20, and 14.4 kDa, top to  
bottom (lane M). TN123 without cross-linking (lane 1). TN123  
cross-linked with DMSI for 15 min. at 37°C, 50°C, 60°C, and  
30 70°C (lanes 2 to 5), respectively. The fusion protein  
H6FXtripb-UB (SEQ ID NO: 31) without cross-linking (lane 6).  
H6FXtripb-UB cross-linked with DMSI for 15 min. at 37°C,  
50°C, 60°C, and 70°C (lanes 7 to 10), respectively and  
H6FXtripb-UB incubated at 70°C for 15 min. (lane 11).

Fig. 13: Construction of the expression plasmid pTH6FXtripb-UB.

The amplified DNA fragment comprising the nucleotide sequence (SEQ ID NO:16) encoding the ubiquitin amino acid sequence (SEQ ID NO: 19) from Q2 to G76 was cut with the restriction enzymes BclI and HindIII and ligated into the BamHI and HindIII sites of the expression plasmid pT7H6FXtripb (Example 1) using standard procedures.

Fig. 14: Predicted amino acid sequence of the fusion protein H6FXtripb-UB (SEQ ID NO: 31) encoded by the expression plasmid pTH6FXtripb-UB.

Fig. 15: Construction of the expression plasmid pTH6FXscFV (CEA6)tripb.

The DNA fragment, amplified with the primer pair SEQ ID NOs: 21 and 22, comprising the nucleotide sequence SEQ ID NO: 20 encoding the single chain antibody CEA6, scFV (CEA6), amino acid sequence from Q1 to A261 was cut with the restriction enzymes BamHI and KpnI and ligated into the BglII and KpnI sites of the expression plasmid pT7H6FXtripb (Example 1) using standard procedures.

Fig. 16: Predicted amino acid sequence of the fusion protein H6FXscFV(CEA6)tripb encoded by the expression plasmid pH6FXscFV(CEA6)tripb.

Fig. 17: Construction of the expression plasmid pTH6FXtripbscFX(CEA6).

The DNA fragment, amplified with the primer pairs having SEQ ID NO: 21 and 23, comprising the nucleotide sequence (SEQ ID NO: 20) encoding the single chain antibody CEA6, scFV (CEA6), amino acid sequence from Q1 to A261 was cut with the restriction enzymes BamHI and HindIII and ligated into the BamHI and HindIII sites of the expression plasmid pT7H6FXtripb (Example 1) using standard procedures.

Fig. 18: Predicted amino acid sequence of the fusion protein H6FXtripbscFv(CEA6) encoded by the expression plasmid pH6FXtripbscFv(CEA6).

Fig. 19: Construction of the expression plasmid

5 pTH6FXscFv(CEA6)tripbscFX(CEA6).

The DNA fragment, amplified with the primer pair SEQ ID NO: 21 and 23, comprising the nucleotide sequence (SEQ ID NO: 20) encoding the single chain antibody CEA6, scFV (CEA6), amino acid sequence from Q1 to A261 was cut with the restriction  
10 enzymes BamHI and HindIII and ligated into the BamHI and HindIII sites of the expression plasmid pT7H6FXscFv(CEA6)tripb (Example 4) using standard procedures.

Fig. 20: Predicted amino acid sequence of the fusion protein H6FXscFv(CEA6)tripbscFv(CEA6) (SEQ ID NO: 34) encoded by the  
15 expression plasmid pH6FXscFv(CEA6)tripbscFv(CEA6).

Fig. 21: Cross-linking analysis of the H6FXtripbscFv(CEA6) fusion protein (SEQ ID NO: 33).

In parallel experiments the fusion proteins H6FXtripbscFv(CEA6) (SEQ ID NO: 33) and TN123 were cross-  
20 linked at room temperature for 30 min. with 0 mg/ml, 0.5 mg/ml, 1.0 mg/ml, 1.5 mg/ml, and 2.0 mg/ml of DMSI, respectively. Lane 1: H6FXtripbscFv(CEA6) without DMSI, H6FXtripbscFv(CEA6) with 0.5 mg/ml DMSI (lane 2), H6FXtripbscFv(CEA6) with 1.0 mg/ml DMSI (lane 3),  
25 H6FXtripbscFv(CEA6) with 1.5 mg/ml DMSI (lane 4) and H6FXtripbscFv(CEA6) with 2.0 mg/ml DMSI (lane 5). Protein marker of 94, 68, 43, 30, 20, and 14.4 kDa, top to bottom (lane M). Lane 6: TN123 without DMSI, TN123 with 0.5 mg/ml DMSI (lane 7), TN123 with 1.0 mg/ml DMSI (lane 8) TN123 with  
30 1.5 mg/ml DMSI (lane 9) and TN123 with 2.0 mg/ml DMSI (lane 10).

DETAILED DISCLOSURE OF THE INVENTION

The term "trimerising structural element" (TTSE) used in the present description and claims is intended to refer to the portion of a polypeptide molecule of the tetranectin family which is responsible for trimerisation between monomers of the tetranectin polypeptide. The term is also intended to embrace variants of a TTSE of a naturally occurring tetranectin family member, variants which have been modified in the amino acid sequence without adversely affecting, to any substantial degree, the trimerisation properties relative to those of the native tetranectin family member molecule. Specific examples of such variants will be described in detail herein, but it is generally preferred that the TTSE is derived from human tetranectin, murine tetranectin, C-type lectin of bovine cartilage, or C-type lectin of shark cartilage. Especially preferred is monomer polypeptide constructs including at least one TTSE derived from human tetranectin.

The 49 residue polypeptide sequence encoded by exons 1 and 2 of tetranectin (Fig. 1) appears to be unique to the tetranectin group of proteins (Fig. 2) as no significant sequence homology to other known polypeptide sequences has been established. In preparation for experimental investigations of the architecture of tetranectin a collection of recombinant proteins was produced, the collection including complete tetranectin, the CRD domain (approximately corresponding to the polypeptide encoded by exon 3), a product corresponding to the polypeptide encoded by exons 2+3, a product corresponding to exons 1+2 (Holtet et al., 1996; Example 2). As detailed in Example 2 we now know differently: tetranectin is indeed a trimer, but the exon 2 encoded polypeptide is in fact capable of effecting trimerisation by itself as evidenced by the observation that the recombinant protein corresponding to exons 2+3 is in fact trimeric in solution.

3D-structure analysis of crystals of full-length recombinant tetranectin (Nielsen et al., 1996; Nielsen, 1996; Larsen et al., 1996; Kastrup, 1996) has shown that the polypeptide

encoded in exon 2 plus three residues encoded in exon 3 form a triple alpha helical coiled coil structure.

- From the combination of sequence and structure data it becomes clear that trimerisation in tetranectin is in fact generated by a structural element (Fig. 2), comprising the amino acid residues encoded by exon two and the first three residues of exon 3 by an unusual heptad repeat sequence, that apparently is unique to tetranectin and other members of its group: This amino acid sequence (Fig. 2) is characterised by two copies of heptad repeats (abcdefg) with hydrophobic residues at a and d positions as are other alpha helical coiled coils. These two heptad repeats are in sequence followed by an unusual third copy of the heptad repeat, where glutamine 44 and glutamine 47 not only substitute the hydrophobic residues at both the a and d position, but are directly involved in the formation of the triple alpha helical coiled coil structure. These heptad repeats are additionally flanked by two half-repeats with hydrophobic residues at the d and a position, respectively.
- The presence of beta-branched hydrophobic residues at a or d positions in alpha helical coiled coil are known to influence the state of oligomerisation. In the tetranectin structural element only one conserved valine (number 37) is present. At sequence position 29 in tetranectin no particular aliphatic residue appears to be preferred.

In summary, it is apparent that the triple stranded coiled coil structure in tetranectin to a large extent is governed by interactions that are unexpected in relation to those characteristic among the group of known coiled coil proteins.

- The TTSEs form surprisingly stable trimeric molecules. (Examples 2, 3 and 4). The experimental observations, that (1) a substantial part of the recombinant proteins exists in the oligomeric state of - and can be cross-linked as - trimeric molecules even at 70°C and (2) that exchange of

monomers between different trimers can only be detected after exposure to elevated temperature are evidence of a extremely high stability of the tetranectin trimerising structural element. This feature must be reflected in the amino acid sequence of the structural element. In particular, the presence and position of the glutamine containing repeat in the sequential array of heptad repeats is, together with the presence and relative position of the other conserved residues in the consensus sequence (Fig. 2), considered important for the formation of these stable trimeric molecules. For most practical uses the cysteine residue 50 should be mutagenized to serine, threonine, methionine or to any other amino acid residue in order to avoid formation of an unwanted inter-chain disulphide bridge, which eventually would lead to uncontrolled multimerisation, aggregation and precipitation of a polypeptide product harbouring this sequence.

In particular in conjunction with the trimer-stabilising exon 1 encoded polypeptide (tetranectin residues 1 to 16, see Example 2), the tetranectin trimerising structural element is a truly autonomous polypeptide module retaining its structural integrity and propensity to generate a highly stable homotrimeric complex whether it is attached or not by a peptide bond at either or at both termini to other proteins. This unique property is demonstrated in the accompanying examples, which provide experimental proof, that polypeptide sequences derived from heterologous proteins may readily be trimerised when joined as fusion proteins to the tetranectin trimerising structural element. This remains valid irrespective of whether the heterologous polypeptide sequences are placed amino-terminally or carboxy-terminally to the trimerising element allowing for the formation of one molecular assembly containing up to six copies of one particular polypeptide sequence or functional entities, or the formation of one molecular assembly containing up to six different polypeptide sequences, each contributing their individual functional property.



Since three TTSEs of naturally occurring human tetranectin forms up a triple alpha helical coiled coil, it is preferred that the stable complex formed by the TTSEs of the invention also forms a triple alpha helical coiled coil.

- 5 The "tetranectin family" are polypeptides which share the consensus sequence shown in Fig. 2 or a sequence which are homologous at sequence level with this consensus sequence. Hence, monomer polypeptide constructs of the invention are preferred which comprise a polypeptide sequence which has at  
10 least 68% sequence identity with the consensus sequence shown in Fig. 2, but higher sequence identities are preferred, such as at least 75%, at least 81%, at least 87%, and at least 92%.

- By the term "heterologous moiety" is herein meant any chemical entity which can be linked covalently to a TTSE and to  
15 which the TTSE is not natively covalently bound. Hence, the heterologous moiety can be any covalent partner moiety known in the art for providing desired binding, detection, or effector properties. The heterologous moiety can be a ligand  
20 binding structure such as a receptor molecule or the ligand binding part of a receptor molecule, an antibody, an antigen binding antibody fragment, or a molecule having antibody characteristics such as e.g. the "diabodies" described in EP-A-0 672 142, or other ligand binding molecules such as  
25 avidin or streptavidin, or a lectin; a toxin such as ricin; a detectable label such as a fluorescence labelled molecule, a radioactively labelled molecule, an enzymatically labelled molecule; an *in situ* activatable substance, such as a molecule which can be induced by a magnetic field or by  
30 radiation to be radioactively or chemically active; an enzyme such as a peroxidase; a radioactive moiety such as a  $\gamma$ -,  $\alpha$ -,  $\beta$ -, or  $\beta^+$ -emitting molecule, e.g. a molecule comprising one or more radioactive isotopes selected from  $^{14}\text{C}$ ,  $^3\text{H}$ ,  $^{32}\text{P}$ ,  $^{33}\text{P}$ ,  $^{25}\text{S}$ ,  $^{38}\text{S}$ ,  $^{36}\text{Cl}$ ,  $^{22}\text{Na}$ ,  $^{24}\text{Na}$ ,  $^{40}\text{K}$ ,  $^{42}\text{K}$ ,  $^{43}\text{K}$ , and any isotopes  
35 conventionally utilized for the purposes of facilitating detection of probes or the purposes of providing localized

radiation so as to effect cell death; a cytokine such as an interferon or a leukotriene; PNA; a non-proteinaceous polymer such as a polymeric alkaloid, 11. a polyalcohol, a polysaccharide, a lipid and a polyamine; a photo cross-linking moiety, i.e. a chemical entity which effects cross-linking upon photo-activation; and a group facilitating conjugation of the monomer polypeptide construct to a target.

The heterologous moiety is preferably covalently linked to the TTSE by via a peptide bond to the N- or C-terminus of the TTSE peptide chain, via a peptide bond to a side chain in the TTSE or via a bond to a cysteine residue, but any way of coupling covalently heterologous material to a polypeptide chain will be useful. The skilled person will know of such possibilities, e.g. by consulting the teachings of WO 95/31540 in this regard which are hereby incorporated by reference.

However, one interesting aspect of the invention relates to a monomer polypeptide construct of the invention comprising two heterologous moieties which are linked via peptide bonds to the N- and C-terminus, respectively. This approach introduces a number of possibilities in terms of e.g. linking larger entities with oligomers of the invention by having specific activities coupled to each end of the monomers (as explained in detail below, the oligomers of the invention may also utilise a version of this principle, where e.g. one N-terminus and one C-terminus of an oligomer are linked via peptide bonds to independent heterologous moieties).

In general, a complex between two or three monomers are described in the following way: three monomers having one TTSE each forms a trimer designated (1+1+1), whereas a dimer formed between a monomer with two TTSEs and a monomer with one TTSE is designated (1+2). Other (undesired) trimers can of course be formed, e.g. (2+2+1), where two TTSEs are not "in use", but it is preferred that the oligomers of the invention use all of their available TTSEs during complex

formation. It should also be noted that the term "monomer polypeptide construct" is meant to designate a single polypeptide chain which may or may not have non-peptide groups coupled covalently to the polypeptide chain, whereas

5 "dimeric polypeptide" or "dimer", "trimeric polypeptide" or "trimer" and "oligomer" (i.e. a dimer or trimer) in the present context are meant to designate non-covalent complexes of monomer polypeptide constructs. I.e., the traditional

10 definitions of monomers and multimers do not apply in the present specification and claims.

The TTSE as exemplified by exon 2 or exons 1 and 2 of human tetranectin, preferably so modified to allow only heterotrimerisation between dissimilar (1+1+1) or (1+2) (cf. the below discussion) subunits may be deployed as a general

15 affinity mediator, which can be coupled chemically to each member of a selection of target molecules. After such conjugation with TTSE the target molecules may be homo- or heterotrimerised as desired for any application. Similar deployment of dimerisation, using as one partner a polypeptide harbour-

20 ing two TTSE sequences in-line, separated by a linker sequence of suitable length and character, may be yet more advantageous, as in such case absolute control of stoichiometry in complex formation would be possible. Thus, an important embodiment of the invention is a monomer

25 polypeptide construct of the invention comprising 2 TTSEs which are covalently linked by a spacer moiety which allows both of the 2 TTSEs to take part in complex formation with a third TTSE not being part of the monomer polypeptide construct, but equally important is the embodiment of the inven-

30 tion where the monomer polypeptide construct comprises one single TTSE, so as to allow trimerisation between three monomers and hence providing the optimum degree of versatility with respect to the number of functional units which can be easily incorporated into one single complex.

35 In the embodiments where two TTSEs are present in the same monomer it is preferred that the spacer moiety has a length

and a conformation which favours complex formation involving both of the two TTSEs which are covalently linked by the spacer moiety. In this way, problems arising from undesired formation of trimers of the formats (2+1+1), (2+2+2), and  
5 (2+2+1) (wherein only one TTSE of each monomer participates in complex formation) can be diminished. Design and preparation of suitable spacer moieties are known in the art and are conveniently effected by preparing fusion polypeptides having the format TTSE<sup>1</sup>-Spacer-TTSE<sup>2</sup>, where the spacer moiety is a  
10 polypeptide fragment (often a relatively inert one), so as to avoid undesired reactions between the spacer and the surroundings or the TTSEs.

One typical scenario, where such modification may be advantageous is the case of immunological detection where a chemical conjugate of an antibody with enzymes such as peroxidase  
15 is used for in situ staining purposes in tissue or on western blots.

A similar, but yet different, application example would be the deployment of TTSE to mediate conjugation of e.g. alkaline phosphatase and an oligonucleotide which would allow in  
20 situ identification of a given mRNA in a tissue sample concurrently with identification of any other mRNA molecule e.g. by interconnection of a second appropriate oligonucleotide and a signalling/visualisation molecule using e.g. the  
25 biotin - avidin/streptavidin affinity pair for conjugation. The point of having two or more selective affinity systems available for conjugating oligonucleotide probes and detector molecules is that as many different sequences may be detected simultaneously as there are affinity sets available.

30 In terms of chemistry required to exploit TTSE as a conjugating affinity-contributing agent, the peptide corresponding to exon 2 will have a sufficient affinity for most purposes, but incorporation of all, or some segment of the exon 1 polypeptide will serve to increase affinity and stability.  
35 The properties of tetranectin mutants in which many of hydro-

philic (e.g. lys and glu) residues that are largely exterior in the coiled coil structure have been replaced with alanine appear similar to the native protein, suggesting that is indeed possible without interfering very much with stability of the trimeric structure to replace all glu, asp and lys residues by a combination of gln, asn, arg or ala, and thereby generate a sequence that, as an N-terminally blocked synthetic peptide, would be very easy to convert into a chemically stable active-ester component, e.g. an N-hydroxy succinimide ester of an acetylated peptide, that could react with (and thereby couple to) any exposed lysine side chain in a target molecule of interest. Such peptide synthesis, activation and coupling chemistry will be readily designed and applied by a person skilled in the art of peptide chemistry, as will indeed any other conjugation chemistry, like the attachment and use of photo-activatable moieties like e.g. phenyl azides.

In conclusion, it seems that the most important structure in native TTSE is the consensus sequence shown in Fig. 2, and that large variations in the polypeptide chain may be allowed. Hence, one advantageous embodiment of the monomer polypeptide construct of the invention is one where at least one amino acid residue selected from the group consisting of amino acid residue nos. 6, 21, 22, 24, 25, 27, 28, 31, 32, 35, 39, 41, 42, is/are substituted by any non-helix breaking amino acid residue, the amino acid residue numbering referring to amino acid residues in SEQ ID NO: 7. All these residues have been shown not to be directly involved in the intermolecular interactions which stabilises the trimeric complex between three TTSEs of native tetranectin monomers and it is therefore expected that these amino acids may be safely substituted with any amino acid which will not have an adverse effect on helix formation (notably proline, which introduces a rigid bend in a polypeptide chain).

Another advantageous embodiment of the monomer polypeptide construct of the invention is one which is free from any free

amino and/or carboxy groups. This would favour synthesis of a TTSE by means of solid or liquid phase peptide synthesis, since there would be no need of introducing any protective groups during peptide synthesis.

- 5 Since the consensus sequence of Fig. 2 is believed important and since this consensus sequence embraces the above-discussed heptad repeat, it is according to the invention preferred that the TTSE comprises a repeated heptad having the formula a-b-c-d-e-f-g (N to C), wherein residues a and d  
10 generally are hydrophobic amino acids. However, since "a" and "d" in the third of the complete heptads of all known members of the tetranectin family are constituted of glutamine, it is most preferred that the TTSE comprises the heptad repeated 3  
15 times and that the last occurrence of the heptad has a glutamine residue corresponding to residues a and d.

- Since exon 2 of native members of the tetranectin family seems to contain the necessary elements to effect stable trimerisation, it is preferred that the monomer polypeptide construct is free of substantial parts of tetranectin which  
20 is encoded by exon 3 and/or lacks substantial parts of tetranectin which is encoded by exon 1. However, since exon 1 encoded material seems to stabilise the trimeric native tetranectin, it is especially preferred that all or part of exon 1 is part of the monomer polypeptide construct, and it  
25 also seems to be rational to include the first three amino acids encoded by exon 3, since these are known to take part of the formation of the native triple alpha helical coiled coil in human tetranectin.

- One particularly interesting embodiment of the invention is  
30 the possibility of designing oriented molecular assemblies, where one or more functional entities are located N-terminally to the trimerising element and one or more functional entities are located C-terminally to the element. Such types of design may be particularly advantageous where a certain  
35 relative ratio is desired among the different functional

entities included in a specific molecular unit. Such type of design may in addition be used if one or more functional entities for either structural or functional reasons appear incompatible within the same construct. Such may be the case  
5 if one or more of the functional entities are expressed by large or bulky protein domains which for steric reasons might prevent formation of the trimeric molecular unit due to sterical constraints.

The possibility of constructing bi-polar three-way fusion  
10 proteins in which one functionality is placed N-terminally to the coiled coil structure and a different functionality is placed C-terminally is additionally advantageous in applications where large spatial separation between the two functionalities are desirable for optimal function. Examples  
15 of such application are e.g. the deployment of binding domains (e.g. antibody-derived binding modules) for recognition and binding to binding sites located at or close to large structures like cell membranes in cases where it is advantageous to allow for binding of the other end of the  
20 trimerised molecule to a different, but also bulky target.

Hence, as discussed above, the oligomers of the invention may be used to join e.g. bulky surfaces by the oligomer according to the invention comprising at least one heterologous moiety which is positioned N-terminally to a TTSE and at least one  
25 heterologous moiety which is positioned C-terminally to a TTSE. The two heterologous moieties can be either part of the same monomer polypeptide construct or parts of two separate monomer polypeptide constructs.

The extraordinarily high stability of any trimer containing  
30 the tetranectin trimerisation module under physiological buffer and temperature condition (i.e. absence of denaturant, temperature not exceeding 40°C) in combination with the ease by which exchange of monomer subunits between trimers can be effected by incubation at moderately elevated temperature or  
35 in the presence of denaturants provide for a unique opportu-

nity to deploy the trimerisation module as a vehicle to allow the construction of "pick-and-mix" conjugates prepared from previously fabricated collections of homotrimeric molecules. To illustrate the versatility of this design opportunity by way of theoretical example, let us assume that (1) a collection of twenty different antibody constructs (e.g. in the format of single-chain Fv) each of its own characteristic binding specificity, has been selected and then turned into homo-trimeric molecules by fusion to a tetranectin trimerisation module, and let us also assume that a set of twenty different effector molecules (e.g. toxin domains) have similarly been prepared and also conjugated to the tetranectin trimerisation module. A user provided with prefabricated collections of twenty different antibody constructs and twenty different toxin constructs - 40 different reagents in all - has the opportunity then to prepare 400 different toxin-antibody conjugates, simply by mixing a first preferred component from one reagent collection with a second preferred reagent from the other collection and then subject this binary mixture to conditions, i.e. gentle heating or incubation with a suitable level of denaturant, to accomplish subunit exchange among all trimeric molecular species in the mixture. After the subunit exchange step the desired heterobifunctional reagent will be present in the mixture as a major component of the mixture and may then be deployed as such to accomplish a given purpose or, alternatively apply a simple purification step to isolate his favoured heterofunctional binary reagent from any remaining mono-functional trimer species by a simple standard protein purification step, easily designed using standard techniques known in the field of protein purification.

A further enhancement of the versatility of the "pick-and-mix" technology may be achieved by including a specific affinity purification tag on each array of trimerisation module - probe/effector/indicator conjugate, fused directly in-line or, alternatively, fused via a cleavable linker (a polypeptide segment containing e.g. a factor  $X_a$  or an



enterokinase recognition/cleavage site) to the affinity tag. More specifically, if each of three libraries were tagged with affinity handles a, b and c, respectively, that were recognised by binding substances A, B and C, respectively, 5 pure heterotrimers, composed of one member of each library, could be obtained in a three-step affinity purification procedure designed to allow selective recovery of only such trimers that exhibit affinity for substances A and B and C. If, for any reason, subsequent removal of the affinity tags 10 were desirable, and the constructs had been prepared to include cleavable linkers, isolation of the pure heterotrimer, liberated from all affinity tags, could be accomplished by three further affinity purification steps, arranged to isolate only material that would bind to neither substance A 15 nor substance B nor substance C.

Obviously, the scope of "pick-and-mix" design of user-preparable heterofunctional complexes apply not only to the formation of binary hetero-functionality, but would apply by logic extension to the formation of ternary hetero-functionality: 20 To envisage the wealth of possibilities that are inherent to the concept of ternary hetero-functionality in a further theoretical example along the lines given above, three sets of reagent collections, each comprising 20 different functional characteristics, i.e. a collection of in toto 60 25 different homotrimers would allow "pick-and-mix" preparation of 8,000 different tri-functional molecules.

The basic tetranectin trimerisation module will, essentially indiscriminately, form homo- and hetero-trimers with any molecule that also contains a trimerisation module. For some 30 applications it may be advantageous to have available specially engineered derivatives of the tetranectin trimerisation module, which have been reengineered to disallow homotrimer formation and hence only allow hetero-trimerisation. Thus, an important embodiment of the monomer polypeptide 35 construct of the invention is constructed/reengineered so as to disfavour formation of complexes between identical TTSEs;

this also has the implication that oligomers of the invention can advantageously be comprised of monomer polypeptide constructs which are designed so as to disfavour formation of trimers including two monomer polypeptide constructs having  
5 identical TTSEs. One way of disfavouring the formation of homotramerisation would be by "knobs into holes" mutagenesis.

The design/reengineering may be accomplished by introduction of amino acid substitution at sites in the polypeptide intimately involved in the formation and stability of the trimer  
10 and, simultaneously, in a different construct introduce a compensatory amino acid substitution, all in all removing symmetry between individual monomer components of the triple helical structure so that the structural complementarity profile only allows the formation of hetero-trimers, but is  
15 incompatible with some or each of the homotrimer species.

A yet different way to deploy the tetranectin trimerisation module as a vehicle to accomplish rational formation of bifunctionalisation would require the interconnection of the C-terminus of one monomer to the N-terminus of a second  
20 monomer in the triple-helical structure. The basic requirement for such an intervening polypeptide is, that allowed spatial distances between its N- and C-termini must be compatible with the spacing inherent to the structural requirements given by the architecture of the tetranectin trimerisation  
25 module. The construction of an intervening connecting polypeptide allowed according to such criteria would be readily accomplished by an average person skilled in the art of protein engineering, as an ample collection of examples of the deployment of, usually flexible, spacer sequences are  
30 known both in nature and in designed proteins. Due to the expected entropic contribution to interaction energy in a molecule in which two of the three tetranectin trimerisation module components are covalently tied together, such a molecule would show great preference for selecting any molecule  
35 containing only a single copy of the tetranectin trimerisa-

tion module component, as this selection would be energetically favoured. Hence, conjugation of one functional protein component to a suitably selected covalently dimerised tetra-nectin trimerisation module component and conjugation of a  
5 different functional protein component to a single-copy element of the trimerisation sequence would provide for the preferential formation of a 1:1 bifunctional complex and suppression of formation of any other complex.

The monomers of the invention may be prepared by methods  
10 generally known in the art, using exclusively or in combination the techniques of recombinant protein production, peptide synthesis (liquid phase or solid phase), and traditional chemical coupling of heterologous moieties to a peptide chain or to specific residues therein. Hence the  
15 invention also relates to a method of preparing the monomer polypeptide construct of the invention, the method comprising

- isolating the monomer polypeptide construct from a culture comprising a host cell which carries and expresses a nucleic acid fragment which encodes the monomer  
20 polypeptide construct,
- synthesizing, by means of chemical peptide synthesis, the monomer polypeptide construct and subsequently isolating the monomer polypeptide construct from the reaction mixture,
- 25 - preparing a TTSE in a culture comprising a host cell which carries and expresses a nucleic acid fragment which encodes the TTSE, subsequently linking covalently at least one heterologous moiety to the TTSE, and thereafter isolating the resulting monomer polypeptide construct, or
- 30 - synthesizing, by means of chemical peptide synthesis, a TTSE, subsequently linking covalently at least one heterologous moiety to the TTSE, and thereafter the

isolating the resulting monomer polypeptide construct from the reaction mixture,

and optionally subjecting the monomer polypeptide construct to further processing.

- 5 The nucleic acid fragment which is mentioned above is also a part of the invention and is defined as a nucleic acid fragment in isolated form which encodes a TTSE as defined herein or which encodes the polypeptide part of a monomer polypeptide construct according to the invention, with the
- 10 proviso that the nucleic acid fragment is different from one that encodes native members of the tetranectin family, and that the nucleic acid fragment is different from one that encodes any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23, the sequences of which are shown in SEQ
- 15 ID NOs: 24-27.

- The above mentioned host cell (which is also a part of the invention) can be prepared by traditional genetic engineering techniques which comprises inserting a nucleic acid fragment (normally a DNA fragment) encoding the polypeptide part of a
- 20 monomer polypeptide construct of the invention into a suitable expression vector, transforming a suitable host cell with the vector, and culturing the host cell under conditions allowing expression of the polypeptide part of the monomer polypeptide construct. The nucleic acid fragment encoding the
- 25 polypeptide may be placed under the control of a suitable promoter which may be inducible or a constitutive promoter. Depending on the expression system, the polypeptide may be recovered from the extracellular phase, the periplasm or from the cytoplasm of the host cell.

- 30 Suitable vector systems and host cells are well-known in the art as evidenced by the vast amount of literature and materials available to the skilled person. Since the present invention also relates to the use of the nucleic acid fragments of the invention in the construction of vectors and in

host cells, the following provides a general discussion relating to such use and the particular considerations in practising this aspect of the invention.

In general, of course, prokaryotes are preferred for the  
5 initial cloning of nucleic sequences of the invention and constructing the vectors useful in the invention. For example, in addition to the particular strains mentioned in the more specific disclosure below, one may mention by way of example, strains such as *E. coli* K12 strain 294 (ATCC No.  
10 31446), *E. coli* B, and *E. coli* X 1776 (ATCC No. 31537). These examples are, of course, intended to be illustrative rather than limiting.

Prokaryotes are also preferred for expression, since efficient purification and protein refolding strategies are  
15 available. The aforementioned strains, as well as *E. coli* W3110 (F-, lambda-, prototrophic, ATCC No. 273325), bacilli such as *Bacillus subtilis*, or other enterobacteriaceae such as *Salmonella typhimurium* or *Serratia marcesans*, and various *Pseudomonas* species may be used.

20 In general, plasmid vectors containing replicon and control sequences which are derived from species compatible with the host cell are used in connection with these hosts. The vector ordinarily carries a replication site, as well as marking sequences which are capable of providing phenotypic selection  
25 in transformed cells. For example, *E. coli* is typically transformed using pBR322, a plasmid derived from an *E. coli* species (see, e.g., Bolivar et al., 1977). The pBR322 plasmid contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells.  
30 The pBR plasmid, or other microbial plasmid or phage must also contain, or be modified to contain, promoters which can be used by the microorganism for expression.

Those promoters most commonly used in recombinant DNA construction include the B-lactamase (penicillinase) and lactose

promoter systems (Chang et al., 1978; Itakura et al., 1977; Goeddel et al., 1979) and a tryptophan (trp) promoter system (Goeddel et al., 1979; EPO Appl. Publ. No. 0036776). While these are the most commonly used, other microbial promoters have been discovered and utilized, and details concerning their nucleotide sequences have been published, enabling a skilled worker to ligate them functionally with plasmid vectors (Siebwenlist et al., 1980). Certain genes from prokaryotes may be expressed efficiently in *E. coli* from their own promoter sequences, precluding the need for addition of another promoter by artificial means.

In addition to prokaryotes, eukaryotic microbes, such as yeast cultures may also be used. *Saccharomyces cerevisiae*, or common baker's yeast is the most commonly used among eukaryotic microorganisms, although a number of other strains are commonly available. For expression in *Saccharomyces*, the plasmid YRp7, for example, is commonly used (Stinchcomb et al., 1979; Kingsman et al., 1979; Tschemper et al., 1980). This plasmid already contains the trp1 gene which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan for example ATCC No. 44076 or PEP4-1 (Jones, 1977). The presence of the trp1 lesion as a characteristic of the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan.

Suitable promoting sequences in yeast vectors include the promoters for 3-phosphoglycerate kinase (Hitzman et al., 1980) or other glycolytic enzymes (Hess et al., 1968; Holland et al., 1978), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. In constructing suitable expression plasmids, the termination sequences associated with these genes are also ligated into the expres-

sion vector 3' of the sequence desired to be expressed to provide polyadenylation of the mRNA and termination.

Other promoters, which have the additional advantage of transcription controlled by growth conditions are the promoter region for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, and the aforementioned glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Any plasmid vector containing a yeast-compatible promoter, origin of replication and termination sequences is suitable.

In addition to microorganisms, cultures of cells derived from multicellular organisms may also be used as hosts. In principle, any such cell culture is workable, whether from vertebrate or invertebrate culture. However, interest has been greatest in vertebrate cells, and propagation of vertebrate in culture (tissue culture) has become a routine procedure in recent years (Tissue Culture, 1973). Examples of such useful host cell lines are VERO and HeLa cells, Chinese hamster ovary (CHO) cell lines, and WI38, BHK, COS-7 293 and MDCK cell lines.

Expression vectors for such cells ordinarily include (if necessary) an origin of replication, a promoter located in front of the gene to be expressed, along with any necessary ribosome binding sites, RNA splice sites, polyadenylation site, and transcriptional terminator sequences.

For use in mammalian cells, the control functions on the expression vectors are often provided by viral material. For example, commonly used promoters are derived from polyoma, Adenovirus 2, and most frequently Simian Virus 40 (SV40). The early and late promoters of SV40 virus are particularly useful because both are obtained easily from the virus as a fragment which also contains the SV40 viral origin of replication (Fiers et al., 1978). Smaller or larger SV40 fragments

may also be used, provided there is included the approximately 250 bp sequence extending from the *HindIII* site toward the *BglI* site located in the viral origin of replication. Further, it is also possible, and often desirable, to utilize  
5 promoter or control sequences normally associated with the desired gene sequence, provided such control sequences are compatible with the host cell systems.

An origin of replication may be provided either by construction of the vector to include an exogenous origin, such as  
10 may be derived from SV40 or other viral (e.g., Polyoma, Adeno, VSV, BPV) or may be provided by the host cell chromosomal replication mechanism. If the vector is integrated into the host cell chromosome, the latter is often sufficient.

15 Upon production of the polypeptide monomer constructs it may be necessary to process the polypeptides further, e.g. by introducing non-proteinaceous functions in the polypeptide, by subjecting the material to suitable refolding conditions (e.g. by using the generally applicable strategies suggested  
20 in WO 94/18227), or by cleaving off undesired peptide moieties of the monomer (e.g. expression enhancing peptide fragments which are undesired in the end product).

In the light of the above discussion, the methods for recombinantly producing the monomer polypeptide construct of the  
25 invention are also a part of the invention, as are the vectors carrying and/or being capable of replicating the nucleic acids according to the invention in a host cell or a cell-line. According to the invention the expression vector can be e.g. a plasmid, a cosmid, a minichromosome, or a  
30 phage. Especially interesting are vectors which are integrated in the host cell/cell line genome after introduction in the host.

Another part of the invention are transformed cells (useful in the above-described methods) carrying and capable of



replicating the nucleic acid fragments of the invention; the host cell can be a microorganism such as a bacterium, a yeast, or a protozoan, or a cell derived from a multicellular organism such as a fungus, an insect cell, a plant cell, or a mammalian cell. Especially interesting are cells from the bacterial species *Escherichia*, *Bacillus* and *Salmonella*, and a preferred bacterium is *E. coli*.

Yet another part of the invention relates to a stable cell line producing the polypeptide part of a monomer polypeptide construct according to the invention, and preferably the cell line carries and expresses a nucleic acid of the invention.

On the basis of the above discussions it will be clear to the skilled person that also the oligomers resulting from the complex formation between the monomer constructs of the invention are important parts of the invention. Hence the invention also pertains to an oligomer which is comprised of two monomer polypeptide constructs according to the invention which comprises at least three TTSEs, or which is comprised of three monomer polypeptide constructs according to the invention which each only contain one single TTSE.

As is explained herein and shown in the examples, the oligomers of the invention are stable at temperatures up to 70°C and it is therefore especially preferred that the oligomers of the invention are stable at temperatures above physiological ones, e.g. that the oligomers are stable in the temperature range 50-70°C.

Also a part of the invention is a method for preparing a dimeric oligomer of the invention which comprises

- admixing a monomer polypeptide construct which includes two TTSEs (construct 1) with a monomer polypeptide construct which includes only one TTSE (construct 2),

- effecting the two TTSE's of construct 1 to complex with the TTSE of construct 2 (this can be done by thermal treatment, i.e. heating to a temperature which ensures denaturation followed by subsequent cooling allowing renaturation, or this can be done by denaturing/renaturing effected by changes in the chemical environment), and
- isolating the resulting dimer and optionally subjecting the dimer to further processing (cf. the above discussion of further processing, but it should also be mentioned that the further processing could include non-covalent coupling of interesting and relevant moieties to the dimeric oligomer).

Consequently, the method for producing a trimeric oligomer is also a part of the invention and comprises the steps of

- admixing three monomer polypeptide constructs of the invention with each other,
- effecting complex formation between one TTSE of each monomer polypeptide construct, and
- isolating the resulting trimer and optionally subjecting the trimeric oligomer to further processing.

The considerations applying to complex formation and further processing mentioned above apply to this method also.

In view of the detailed discussion above of the "pick-and-mix" aspect of the invention, the invention also pertains to a kit comprising

- a first package comprising at least one container means, each at least one container means containing a monomer polypeptide construct of the invention,

- a second package comprising at least one container means, each at least one container means in the second package containing a monomer polypeptide construct of the invention, the second package being different from the first package with respect to choice and/or number of monomer polypeptide constructs included therein, and optionally
- a third package comprising at least one container means, each at least one container means in the third package containing a monomer polypeptide construct of the invention, the second package being different from the first and second packages with respect to choice and/or number of monomer polypeptide constructs included therein.

It is preferred that the at least one container means in each package contains mutually distinct monomer polypeptide constructs, and it is especially preferred that all container means comprised in the kit comprises mutually distinct polypeptide constructs.

A very important aspect of the invention is the possibility of generating a system designed especially for the individual circumstances. The basic idea is that the artificial selection of heterologous moieties and optionally active components, and functional entities result in a unique system as will be further disclosed in the following.

Using the TTSE as a vehicle for assembling monovalent scFv or Fab antibody fragments into oligomeric and multivalent entities offer design advantages also in terms of generating chimaeric artificial antibodies having desirable pharmacokinetic and pharmacodynamic properties. Small derivatives like monomeric scFv fragments or bivalent "minibodies" are rapidly cleared from the circulatory system, whereas complete Igs stay for very much longer. Conversely, small derivatives like scFv and minibodies exhibit better extravasation properties. It is therefore expected that antibodies of a desired specificity may be optimized for

particular diagnostic or therapeutic needs by engineering the pharmacological properties, using the TTSE as a vehicle for controlled oligomerization of e.g. scFv fragments.

One example of such engineering would be the requirements for  
5 delivering a high dose of an imaging or toxin-conjugated antibody to a tumour, while ensuring as low a systemic exposure or imaging background as possible. In such case a TTSE conjugated scFv fragment could be designed to exhibit strong multivalent binding to the tumour and rapid clearance  
10 of excess conjugate from circulation.

Accordingly, in af further aspect the present invention also relates to the use of a monomer polypeptide construct or to a an oligomer according to the present invention as a vehicle for assembling antibody fragments into oligomeric or  
15 multivalent entities for generating chimeric artificial antibodies having preselected pharmacokinetic and/or pharmadynamic properties.

The use of specific delivery systems also play an important role in connection with the present invention in that such  
20 systems may by utilized with respect to different use of the present invention both with respect to the a more general therapeutic application and with respect to gene therapy. Exampls of suitable drug delivery and targeting systems are disclosed in Nature 392 supp.(30 april 1998).

Accordingly, efficiency of deliverance may be further increased if the delivery system e.g a liposome is supplied with a molecular unit, an "infector or transfactor" ligand, recognized by a internalizing receptor unit specific for the target cells. For example, cells displaying endocytotic  
25 receptors like members of the LDL family of receptors may be even more efficiently infected or transfected either by including a TTSE unit in the antibody containing heteorimer or in an independent TTSE unit conjugated to one or more of the domains of the Receptor Associated Protein, RAP,  
30

(Ellgaard, L., Holtet, T.L., Nielsen, P.R., Etzerodt, M., Gliemann, J. & Thøgersen, H.C. Eur J Biochem. 1997, vol 244, 544-551) which is recognized as a ligand to all receptors in this abundant family of endocytosis-mediating receptors.

- 5 Accordingly, in a further aspect, the invention is directed to the use of a monomer polypeptide construct or to an oligomer according to the invention for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of cells.
- 10 The ultimate perspective of such TTSE-mediated gene therapy would be the deployment of a viral vector that would find no other targets in the patient but the cells displaying the artificial receptor complex.

- 15 In a still further aspect, the invention is directed to the use of a monomer polypeptide construct or to a an oligomer construct according to the invention wherein the at least one heterologous moiety comprises a moiety selected from a ligand binding structure such as a receptor molecule or the ligand binding part of a receptor molecule, and wherein the gene
- 20 therapy involves the delivery of nucleic acids to the desired population of cells by use of a viral vector directed to cells displaying the artificial receptor complex corresponding to the heterologous moiety.

- 25 In another aspect, the invention is directed to the use of a monomer polypeptide construct or to a an oligomer construct according to the invention wherein at least one TTSE is modified with a membrane integrating or associating entity having affinity to the specific population of cells in the body relevant for the gene therapy.

- 30 Furthermore, a recent review of the imaging an therapeutic potential of a range of known antibody derivatives has been published by Paul Carter and Margaret Merchant of Genentech Inc. (Current Opinion in Biotechnology, 1997, vol 8, 449-

454). In direct continuation of their conclusions it will be apparent that oligomerisation of antibody derivatives like scFv derivatives may extend current technology in the designer-antibody field in many important aspects, some of which will be elaborated below (with reference to the Carter & Merchant review).

One of the well-known problems inherent to mouse monoclonal antibodies that have been 'humanized' by grafting of the murine antigen combining site onto a human Ig framework is that antigenicity of the chimaeric product in human patients is often difficult to suppress entirely, resulting in - sometimes life-threatening - immune reactions to the diagnostic or therapeutic humanized antibody product. The risk of such side-effects are expected to be much reduced if the designer antibody is assembled from purely human proteins or protein fragments. Since the TTSE trimerising unit described here is identical to a portion of human tetranectin that is already present in human plasma and tissue, there is good reason to expect that the TTSE will not elicit an antigenic response in a human subject if it is introduced as a component of a chimaeric product that is not otherwise antigenic in humans.

Accordingly, in one aspect, the present invention relates to the use of a monomer polypeptide construct or to a an oligomer according to the present invention as a component of a chimaeric product having low antigenicity in humans relative to formulations comprising on or more components of non-human origin.

Carter & Merchant further review present technology for radiolabelling of antibody derivatives. Again, oligomerisation using TTSEs offer more elegant solutions to problems associated with labelling, as the TTSE offers the possibility to construct one or two of the TTSE monomer units in a heterotrimeric complex to harbour the site carrying the label. Thus, in this format labelling may also be confined to

the non-antibody part of the complex, leaving the antigen-binding module entirely unmodified, and the complex may furthermore be formulated "in the field" as and when needed.

In many receptor-mediated signal transduction pathways

5 signals are triggered by the clustering of receptor molecules on the cell membrane. The TTSEs therefore have important applications in the study and exploitation of receptor signalling, as ligands may be presented as oligomers by conjugation to a TTSE unit.

10 This also has important application in phage display technologies for discovering new ligands and new receptors as the engineering of a TTSE unit fused inline to a candidate ligand molecule will allow the display of a hetero-trimeric phage coat protein, in which only one of the monomer units is  
15 conjugated to the phage coat protein. This may be accomplished by appropriate insertion of amber codons at the site of fusion of phage coat protein to the TTSE-ligand segment of the three-way fusion protein encoded by the recombinant phage. In appropriate E. coli cells the presence  
20 of this amber codon will result in translation termination in the majority of read-throughs, and hence most of the fusion protein product secreted to the periplasmic compartment in the phage-infected bacterium will be soluble TTSE-ligand fusion protein, whereas a minority of the fusion protein will  
25 also contain a phage protein module. The majority of trimers that will be generated will therefore contain, at most, one monomeric unit that will ensure integration (display) in the mature recombinant phage particle.

A further advantage of the display technology described above  
30 relates to the fact that it is specially useful for selection on the basis of a relatively low affinity because of the entropic benefit contribution obtained by the proximity of the two binding moieties in confined spatial arrangement.

Accordingly, the present invention in an important aspect, also relates to protein library technology wherein the TTSE's discribed above are utilized.

The trimerisation of candidated recombinant ligands is especially important as, for many receptors, the intracellular signal is induced by receptor clustering, which is only brought about if the external ligand exhibits multivalent binding to the receptor, so as to bridge two or more receptor molecules.

- 10 In one preferred embodiment the monomer polypeptide construct or the oligomer construct according to the invention is for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of cells. Tthe at least one heterologous moiety may
- 15 comprise a moiety selected from a ligand binding structure such as a receptor molecule or the ligand binding part of a receptor molecule, and wherein the gene therapy involves the delivery of nucleic acids to the desired population of cells by use of a viral vector directed to cells displaying the
- 20 artificial receptor complex corresponding to the heterologous moiety.

- As mentioned above, it is an important aspect of the invention that the monomer polypeptide construct and/or the oligomer may be used as a component of a chimaeric product
- 25 having low antigenicity in humans. As the construct is of human origin it is believed that the antigenicity in humans is low relative to formulations comprising on or more components of non-human origin.

- One primary use of a monomer polypeptide construct or a an oligomer according to the invention is for delivering an
- 30 imaging or toxin-conjugated antibody to a target such as a tumor, or use as a vehicle delivering an substance to a target cell or tissue, as a vehicle for assembling antibody fragments into oligomeric or multivalent entities for



generating chimeric artificial antibodies having preselected pharmacokinetic and/or pharmacodynamic properties.

The substance in question being one or more selected from the group of heterologous moities as well a pharmaceutical. Also  
5 a labelled construct wherein the label is coupled to one or to of the TTSE monomer units is within the scope of the invention.

As explained in detail previously, an important and surprising use of the monomer polypeptide construct or the  
10 oligomer according to the pesenent invention is for protein library technology, such as phage display technology. The present invention also relates to any polynucleotid molecule such as a RNA, DNA or PNA as well as any vector encoding one or more TTSE.

15 A further use according to invention includes preparation and use of a pharmaceutical composition comprising the TTSE construct and optionally a pharmaceutically acceptable excipient. The composition may be administered by a route selected from the group consisting of the intravenous route,  
20 the intraarterial route, the transmembraneus route of the buccal, anal, vaginal or conjunctival tissue, the intranasal route, the pulmonary route, the transdermal route, the intramuscular routed, subcutaneous route, intratechal route, inoculation into tissue such as a tumour, or by an implant.

25 The the monomer polypeptide construct or the oligomer is in a preferred embodiment comprised in a liposome.

It is obvious from the disclosure of the present invention that the treating or preventing of a disease may by a further aspect comprising administering to the subject in need  
30 thereof an effective amount of a pharmaceutical composition referred to above.

In one aspect of the various possibilities according to the present invention concerning how the human gene therapy is targeted, includes the case wherein at least one TTSE is modified with a membrane integrating or associating entity  
5 having affinity to the specific population of cells in the body relevant for the gene therapy.

As used in the conventional pharmaceutical field the present invention includes a method wherein the monomer polypeptide construct or the oligomer is administered by a route selected  
10 from the group consisting of the intravenous route, the intraarterial route, the transmembrane route of the buccal, anal og vaginal tissue, intranasal route, the pulmonary route, the transdermal route, intramuscular, subcutaneous, intratechal, the buccal, inoculation into tissue such as a  
15 tumour, or by an implant.

Finally, the present invention is also relating to the field of dianosing as the skilled person would easily recognise, that the TTSE disclosen in the present inventiion may also refer to a method for diagnosis comprising a construct  
20 comprising the monomer polypeptide construct or the oligomer, together with a diagnosing component coupled thereon.

#### EXAMPLE 1

*Design and construction of the pTH6trip E. coli expression vectors for the production of trimerised chimeric fusion  
25 proteins.*

The plasmid clone pT7H6FXTN123 (Example 2) was used as template for amplification in two Polymerase Chain Reactions (PCR) (Saiki et al., 1988) with the primer pairs trip-N (SEQ ID NO: 1) and trip-Ca (SEQ ID NO: 2) and trip-N (SEQ ID NO: 30 1) and trip-Cb (SEQ ID NO: 3), respectively. The amplified DNA fragments, tripa, comprising nucleotide sequences encoding an IQGR cleavage site for the restriction protease FX<sub>a</sub>

(SEQ ID NO: 4) followed by two sites for the restriction nucleases BglII and KpnI, the nucleotide sequence encoding the tetranectin polypeptide sequence for Glu 1 to Lys 52 (SEQ ID NO: 5) followed by recognition sites for the three restriction endonucleases BamHI, HindIII, and EcoRI, respectively, and tripb, comprising nucleotide sequences encoding an IQGR cleavage site for the restriction protease FX<sub>a</sub> (SEQ ID NO: 4) followed by two sites for the restriction nucleases BglII and KpnI, the nucleotide sequence encoding the tetranectin polypeptide sequence for Glu 1 to Val 49 (SEQ ID NO: 6) followed by recognition sites for the three restriction endonucleases BamHI, HindIII, and EcoRI, respectively, were subcloned into the plasmid pT7H6 (Christensen et al., 1991), yielding pTtripa and pTtripb, respectively (Figs. 3 and 4).

## EXAMPLE 2

*Tetranectin, localisation of the trimerising structural element and stability of the triple alpha helical coiled coil.*

The cDNA encoding the reading frame corresponding to the mature tetranectin single chain (SEQ ID NO: 7) was cloned by specific amplification in a Polymerase Chain Reaction (PCR) (Saiki et al., 1988) of the nucleotide sequences from amino acid residue Glu1 to Val181 using 1<sup>st</sup> strand oligo-dT primed cDNA synthesized from total human placental RNA as template. Primers used in the PCR were SEQ ID NO: 8 and SEQ ID NO: 9. RNA extraction and cDNA synthesis were performed using standard procedures. The amplified reading frame encoding the monomer subunit of tetranectin was at the 5'-end, via the PCR-reaction, linked to nucleotide sequences encoding the amino acid sequence SEQ ID NO: 10 which constitute an IEGR cleavage site for the bovine restriction protease FX<sub>a</sub> (Nagai, and Thøgersen, 1987). A glycine residue was, due to the specific design of the 5'-PCR primer (SEQ. ID NO. 8), inserted between the C-terminal arginine residue of the FX<sub>a</sub> cleavage site (SEQ ID NO. 10) and the tetranectin Glu1-resi-

due. The amplified DNA fragment was subcloned into the *E. coli* expression vector pT<sub>7</sub>H<sub>6</sub> (Christensen et al., 1991) producing the plasmid pT<sub>7</sub>H<sub>6</sub>FX-TN123 expressing the tetranectin monomer H6FXTN123 (SEQ ID NO: 25) and into pT<sub>7</sub>CIIH<sub>6</sub>,

- 5 which is a derivative of pT<sub>7</sub>H<sub>6</sub>, where the amino-terminal 32 amino acid residues of the lambda CII protein (SEQ ID NO. 11) are inserted 5' of the six histidine residues (SEQ ID NO. 12) as outlined in Fig. 5, yielding pT<sub>7</sub>CIIH<sub>6</sub>FX-TN123 expressing the tetranectin fusion protein CIIH6FXTN123 (SEQ ID NO: 24).
- 10 The amino acid sequence of the expressed proteins are shown in Fig. 6 (in SEQ ID NO: 7 is given the amino acid sequence of the mature tetranectin protein). Furthermore three additional derivatives of tetranectin were constructed (Fig. 8): H6FXTN12 comprising the tetranectin amino acid residues Glu1
- 15 to Val49 (SEQ ID NO: 6), H6FXTN23 comprising the tetranectin amino acid residues Val17 to Val181 (SEQ ID NO: 7), and H6FXTN3 (SEQ ID NO: 30) comprising the tetranectin amino acid residues Ala45 to Val181 (SEQ ID NO: 7). These three tetranectin derivatives were constructed by specific amplification
- 20 in a PCR using pT<sub>7</sub>H<sub>6</sub>FX-TN123 as template and the primer-pairs SEQ ID NO: 8 and SEQ ID NO: 13, SEQ ID NO: 14 and SEQ ID NO: 9, and SEQ ID NO: 15 and SEQ ID NO: 9, respectively. The amplified DNA fragments were subcloned into the *E. coli* expression vector pT<sub>7</sub>H<sub>6</sub> producing the plasmids pT<sub>7</sub>H<sub>6</sub>FX-TN12,
- 25 pT<sub>7</sub>H<sub>6</sub>FX-TN23, and pT<sub>7</sub>H<sub>6</sub>FX-TN3, respectively (Fig. 7).

To prepare recombinant tetranectin and its derivatives, each of the plasmids pT<sub>7</sub>H<sub>6</sub>FX-TN123, pT<sub>7</sub>CIIH<sub>6</sub>FX-TN123, pT<sub>7</sub>H<sub>6</sub>FX-TN12, pT<sub>7</sub>H<sub>6</sub>FX-TN23, and pT<sub>7</sub>H<sub>6</sub>FX-TN3 were grown in medium scale (4 x 1 litre; 2xTY medium, 5 mM MgSO<sub>4</sub> and 100 µg ampicillin) in *E.*

30 *coli* BL21 cells, as described by Studier et al. (1990). Exponentially growing cultures at 37°C were at OD<sub>600</sub> 0.8 infected with bacteriophage lambda CE6 at a multiplicity of approximately 5. Cultures were grown at 37°C for another three hours and the cells harvested by centrifugation.

- 35 Cells were resuspended in 150 ml of 0.5 M NaCl, 10 mM Tris-HCl pH 8, and 1 mM EDTA pH 8. Phenol (100 ml adjusted to

pH 8) was added and the mixture sonicated to extract the total protein. Protein was precipitated from the phenol phase by 2.5 volumes of ethanol and centrifugation.

The protein pellet was dissolved in a buffer containing 6M  
5 guanidinium chloride, 50 mM Tris-HCl pH 8 and 0.1 M dithioerythriol. Following gel filtration on Sephadex G-25 (Pharmacia, Sweden) into 8 M Urea, 1 M NaCl, 50 mM Tris-HCl pH 8 and 10 mM 2-mercaptoethanol, the crude protein preparation was applied to a  $\text{Ni}^{2+}$  activated NTA-agarose column ( $\text{Ni}^{2+}$ NTA-aga-  
10 rose, 75 ml pre-washed with 8 M urea, 1 M NaCl, 50 mM Tris-HCl pH 8, and 10 mM 2-mercaptoethanol) for purification (Hochuli et al., 1988) and refolding of the fusion proteins, H6FXTN123, CIIH6FXTN123, H6FXTN12, H6FXTN23, and H6FXTN3.

For this study we chose to prepare our own  $\text{Ni}^{2+}$ NTA-agarose  
15 matrix. A carbodiimide coupling of the N-(5-amino-1-carboxypentyl) iminodiacetic acid metal ligand (synthesis route as described by Döbeli & Hochuli (EP-A-0 253 303)) to a rigid agarose matrix (Sephacrose CL-6B, Pharmacia, Sweden) was performed:

20 8 g of N-(5-amino-1-carboxypentyl)iminodiacetic acid from the synthesis procedure in 50 ml was adjusted to pH 10 by addition of 29 g of  $\text{Na}_2\text{CO}_3$  (10  $\text{H}_2\text{O}$ ) and added to a stirred suspension of activated Sepharose CL-6B in 1 M  $\text{Na}_2\text{CO}_3$ . Reaction was allowed overnight. The Sepharose CL-6B (initially 100 ml  
25 suspension) was activated after removal of water by acetone with 7 g of 1,1'-carbonyldiimidazol under stirring for 15 to 30 min. Upon activation the Sepharose CL-6B was washed with acetone followed by water and 1 M  $\text{Na}_2\text{CO}_3$ .

The NTA-agarose matrix was loaded into a column and "charged"  
30 with  $\text{Ni}^{2+}$  by slowly passing through 5 column volumes of a 10%  $\text{NiSO}_4$  solution. The amount of  $\text{Ni}^{2+}$  on the NTA-agarose matrix, prepared by this procedure, has been determined to 14  $\mu\text{mol}$  per ml matrix. After charging the  $\text{Ni}^{2+}$ NTA-agarose column was washed with two column volumes of water, one column volume of

1 M Tris-HCl pH 8 and two column volumes of loading buffer before stirred mixing of the  $\text{Ni}^{2+}$ NTA-agarose matrix with the crude protein extracts in a breaker for 15 to 30 min. All buffers prepared for liquid chromatography were degassed  
5 under vacuum prior to addition of reductant and/or use.

The  $\text{Ni}^{2+}$ NTA-agarose matrix - crude extract mixture was packed in standard glass columns for liquid chromatography (internal diameter: 2.6 cm) to a volume of approximately 40 ml. The columns were washed with 200 ml of 8 M urea, 1 M NaCl, 50 mM  
10 Tris-HCl pH 8, and 10 mM 2-mercaptoethanol (Buffer I) and 100 ml 6 M guanidinium chloride, 50 mM Tris-HCl pH 8 and 10 mM 2-mercaptoethanol (Buffer II) and the adsorbed tetranectin derived fusion proteins H6FXTN123, H6CIIFXTN123, H6FXTN23, and H6FXTN3 refolded using the cyclic refolding procedure as  
15 described (Thøgersen et al., WO 94/18227).

The fusion protein H6FXTN12 was refolded by removing the guanidinium chloride and 2-mercaptoethanol of buffer II in a gradient over 5 column volumes into 50 mM Tris-HCl pH 8 and 0.5 M NaCl. After completion of the refolding procedures the  
20 tetranectin derived fusion proteins were eluted from the  $\text{Ni}^{2+}$ NTA-agarose columns with a buffer containing 0.5 M NaCl, 50 mM Tris-HCl, 25 mM EDTA pH 8. The tetranectin fusion proteins H6FXTN123, H6FXTN23, and H6FXTN3 were cleaved with  $\text{FX}_a$  at 4°C overnight in a molar ratio of 1:300. After  $\text{FX}_a$   
25 cleavage the protein samples were concentrated 10 fold by ultrafiltration on YM10 membranes (Amicon). After ten times dilution of the protein sample with 2 mM  $\text{CaCl}_2$ , the recombinant tetranectin derivatives TN123, TN23, and TN3 were isolated by ion-exchange chromatography on Q-Sepharose (Pharmacia, Sweden) in a linear gradient over 10 column volumes from  
30 10 mM Tris-HCl pH 8, 2 mM  $\text{CaCl}_2$  to 10 mM Tris-HCl pH 8, 2 mM  $\text{CaCl}_2$ , and 0.5 M NaCl. After elution from the  $\text{Ni}^{2+}$ NTA-agarose columns the fusion proteins H6CIIFXTN123 and H6FXTN12 were likewise concentrated 10 fold by ultrafiltration on YM10  
35 membranes and gelfiltrated into buffer containing 25 mM Tris-HCl pH 8, 25 mM NaCl, and 2 mM  $\text{CaCl}_2$ , before purification of

correctly folded monomer by ion-exchange chromatography on Q-Sepharose as described.

Recombinant full length tetranectin (TN123) produced by these procedures have been analyzed with respect to binding to plasminogen kringle 4 and immobilised fucoidan, expression of antigenic sites, and localization of disulphide bridges. In all criteria tested the produced TN123 behaved identically to isolated naturally human tetranectin (data not shown). Furthermore TN123 and TN3 have been crystallized (Kastrup et al., 1996) and the structure has also been determined, all of which bear evidence that a single unique and biologically active folded product had indeed been produced.

#### *Analytical gelfiltration analysis of rTN proteins.*

Analytical gelfiltration of the recombinant tetranectin derivatives TN123, TN3, and TN23 (Fig. 9) were performed on a Superose 12 HR 10/30 column (Pharmacia, Sweden) with a total volume of 25 ml in 100 mM NaCl and 50 mM Tris-HCl pH 8 and a flow rate of 0.2 ml/min. The  $K_{av}$  value is defined by,  $K_{av} = (V_e - V_o) / (V_c - V_o)$ .

The gelfiltration analysis of TN123 and TN23 show that both proteins are exclusively found as trimers in solution ( $K_{av}$  values of 0.27 and 0.29, respectively), whereas TN3 appeared monomeric ( $K_{av}$ :0.41).

#### *Chemical cross-linking of tetranectin and derivatives*

The recombinant tetranectin derivatives TN123, TN3, and TN23, together with the fusion proteins CIIH6FXTN123 and H6FXTN12 or mixtures of these derivatives at 1 mg/ml concentrations in cross-linking buffer (0.1 M Sodium borate, pH 9.1) were incubated with dimethylsuberimidate (DMSI, Sigma). 10  $\mu$ l aliquots of protein solution were incubated with 1  $\mu$ l aliquots of DMSI stock solution (20 mg/ml in cross-linking buffer) for 30 minutes at 25°C before addition of 2  $\mu$ l quenching

buffer (3 M Tris-HCl, pH 9). Subunit exchange between pre-formed homo-oligomers was induced by subjecting protein mixtures to heat shock treatment. Five  $\mu$ l aliquots of each protein solution (1 mg/ml stocks) were mixed at 0°C in standard polypropylene microcentrifuge tubes, transferred to a water bath at 70°C for the time spans indicated, and then further incubated for 15 minutes at 25°C before reaction with DMSI.

- 10 Prior to analysis by SDS-PAGE (12% gels) of the cross-linked products the reaction samples were boiled in the presence of SDS and mercaptoethanol.

Cross-linking analysis of TN123 and the fusion protein CIIH6FXTN123 showed that no detectable subunit exchange between pre-formed homo-oligomers in a mixture of TN123 and CIIH6FXTN123 was found after 16 hours at room temperature (Fig. 10). Subunit exchange could be induced by incubating the protein mixture at 70°C for 15 seconds or longer before cooling to room temperature and addition of DMSI. SDS-PAGE analysis showed the presence of four trimer bands above 95 kDa (corresponding to two homo-trimers and two hetero-trimers) and three dimer bands (corresponding to two homo-dimers and one hetero-dimer) in the gel between 43 and 55 kDa, in a relative abundance in agreement with random association of monomer subunits into trimers after subunit exchange. It should be noted, that molecular weight markers have only been included on the SDS-PAGE gels for crude calibration and orientation of the gels.

The trimeric organization of tetranectin was further corroborated by cross-linking studies of the proteins H6FXTN12, TN23, and TN3 and mixtures between them (Fig. 11). The tetranectin derivative TN3, containing only the CRD, could not be cross-linked even at high protein concentrations and did not interfere with the cross-linking of rTN123. Likewise, the derivative TN23, containing exon 2 and the CRD, appeared monomeric after cross-linking and was found not to interfere



with trimerisation of TN123 during subunit exchange. Dimeric TN23 molecules found at low abundance in the sample probably reflects contaminating misfolded disulphide bridged dimers. The fusion protein H6FXTN12 formed homo-trimers upon cross-linking and generated hetero-trimers with TN123 after subunit exchange. Because of the difference in size of full length tetranectin (TN123) and H6FXTN12 the possible nine protein bands resulting from chemical cross-linking are: The four trimers [(TN123)<sub>3</sub>, (TN123)<sub>2</sub>(H6FXTN12), (TN123)(H6FXTN12)<sub>2</sub>, and (H6FXTN12)<sub>3</sub>] at approx. 95 kDa, 50 kDa, 37 kDa, and 20 kDa, respectively; the three dimers [(TN123)<sub>2</sub>, (TN123)(H6FXTN12), and (H6FXTN12)<sub>2</sub>] at approx. 45 kDa, 30 kDa, and 15 kDa, respectively; and the two monomers TN123 at 23 kDa and H6FXTN12 at 9 kDa.

Taken together, the gel filtration and the cross-linking analysis of the tetranectin derivatives show that tetranectin, like the collectin group of C-type lectins, is a trimeric molecule and that amino acid residues directly shown to be involved in trimerisation of the tetranectin monomer are located in exon 2 of the protein (Val17 - Val49). Furthermore subunit exchange between the trimeric molecules could only be observed after heat denaturation. Amino acid residues Glu1 to Asp16 of tetranectin are critical to chemical cross-linking with DMSI and more important appear to stabilize the trimeric molecule because the cross-linking analysis of the mixture TN123 and TN23 showed no decrease in TN123 formation after heat denaturation and possible subunit exchange (Fig. 11). The stability of the tetranectin trimer was corroborated by a cross-linking analysis with DMSI at different temperatures. Fifteen  $\mu$ l TN123 at 0.3 mg/ml concentration was pre-incubated 10 min. at either 37°C, 50°C, 60°C, or 70°C before addition of 2  $\mu$ l DMSI (20 mg/ml). The reaction was allowed to proceed for 15 min. before reaction was quenched with 5  $\mu$ l of 3M Tris-HCl pH 9.1 and the reaction mixtures allowed to cool to room temperature. SDS-PAGE analysis of reduced samples (Fig. 12) showed, that trimers are readily detectable even at 60°C, although a competing pattern

of cross-linking specimens increases at increasing temperatures. The appearance of other cross-linking specimens is probably due to the unfolding of the CRD. The stability of the tetranectin trimerising structural element is further  
5 analyzed using a designed chimeric protein in Example 3.

### EXAMPLE 3

*Design and construction of the recombinant chimeric protein TRIPB-UB - the tetranectin trimerising structural element and ubiquitin.*

10 A plasmid clone, pLCMHF/UB, generously provided by Dr. O. Wiborg harbouring a human ubiquitin cDNA insert (SEQ ID: 16) was used as template and SEQ ID NO: 17 together with SEQ ID NO: 18 were used for amplification in a Polymerase Chain  
15 Reaction (PCR) (Saiki et al., 1988) of the nucleotide sequence encoding amino acid residue Ile1 to Gly76 of human ubiquitin (SEQ ID: 19). The amplified DNA fragment was after digestion with the restriction endonucleases BamHI and HindIII ligated into the BamHI and HindIII sites of pTtripb  
20 (Example 1) yielding pTtripb-UB (Fig. 13) using standard procedures.

To prepare the chimeric fusion protein H6FXtripb-UB (Fig. 14, SEQ ID NO: 31) the plasmid pTtripb-UB was grown in medium  
scale (4 x 1 litre; 2xTY medium, 5 mM MgSO<sub>4</sub> and 100 µg ampicillin) in *E. coli* BL21 cells, as described by Studier et  
25 al. (1990). Exponentially growing cultures at 37°C were at OD<sub>600</sub> 0.8 infected with bacteriophage lambda CE6 at a multiplicity of approximately 5. Cultures were grown at 37°C for another three hours and the cells harvested by centrifugation. Cells were resuspended in 150 ml of 0.5 M  
30 NaCl, 10 mM Tris-HCl pH 8, and 1 mM EDTA pH 8. Phenol (100 ml adjusted to pH 8) was added and the mixture sonicated to extract the total protein. Protein was precipitated from the phenol phase by 2.5 volumes of ethanol and centrifugation. The protein pellet was dissolved in a buffer containing 6 M

guanidinium chloride, 50 mM Tris-HCl pH 8 and 0.1 M dithioerythriol. Following gel filtration on Sephadex G-25 (Pharmacia, Sweden) into 8 M Urea, 1 M NaCl, 50 mM Tris-HCl pH 8 and 10 mM 2-mercaptoethanol, the crude protein preparation was  
5 applied to a  $\text{Ni}^{2+}$  activated NTA-agarose column for purification (Hochuli et al., 1988) and refolding of the fusion protein H6FXtripb-UB.

Synthesis and charging of the  $\text{Ni}^{2+}$  activated NTA-agarose matrix is described in Example 2. All buffers for liquid  
10 chromatography were degassed prior to use. The fusion protein H6FXtripb-UB was refolded by removing the urea and 2-mercaptoethanol from buffer II in a gradient over 5 column volumes into 50 mM Tris-HCl pH 8 and 0.5 M NaCl. After completion of the refolding procedure the H6FXtripb-UB fusion protein was  
15 eluted from the  $\text{Ni}^{2+}$ NTA-agarose columns with a buffer containing 0.5 M NaCl, 50 mM Tris-HCl, 25 mM EDTA pH 8 and gel filtrated on a Sephadex G50 column (Pharmacia) into 0.1 M Sodium borate pH 9 buffer for chemical cross-linking analysis with DMSI.

20 The cross-linking analysis experiment was designed both to analyze the oligomeric status of the chimeric fusion protein and the thermal stability of the presumed fusion protein trimer as described in Example 2: Samples of 15  $\mu\text{l}$  H6FXtripb-UB fusion protein, at approximately 1.0 mg/ml concentration,  
25 were pre-incubated 10 min. at either 37°C, 50°C, 60°C, or 70°C before addition of 2  $\mu\text{l}$  DMSI (20 mg/ml). The reactions were allowed to proceed for 15 min. before quenching by addition of 5  $\mu\text{l}$  of 3 M Tris-HCl pH9.1 and the reaction mixtures were allowed to cool to room temperature. SDS-PAGE  
30 analysis of reduced samples (Fig. 12) showed, (1) that the fusion protein H6FXtripb-UB is a trimer in solution (monomer at 17 kDa, dimer at 35 kDa, and trimer at 43 kDa) and (2) that a substantial amount of trimer molecules is present even at 70°C. The appearance of other larger cross-linking products is probably due to cross-linking of trimers via the  
35 ubiquitin part of the fusion protein.

## EXAMPLE 4

*Design and construction of trimerised and hexamerized CEA6 scFv antibodies scFv(CEA6)-TRIPB, TRIPB-scFv(CEA6) and scFv(CEA6)-TRIPB-scFv(CEA6).*

- 5 A plasmid clone, pUC19MCH/CEA6, generously provided by Dr. Kevin Pritchard, Cambridge Antibody Technology Ltd., Melbourne, UK, harbouring a nucleotide sequence (SEQ ID: 20) encoding the CEA6 antibody in single-chain Fv (scFv) format, followed in sequence by a "myc tag" (which is a general  
10 purification/detection handle), was used as template in Polymerase Chain Reactions (PCR) (Saiki et al., 1988) in which the nucleotide sequence encoding the scFv + myc tag was amplified using the primer pairs (SEQ ID: 21 and SEQ ID: 22) and (SEQ ID: 21 and SEQ ID: 23) to generate PCR fragments "A"  
15 and "B".

- PCR fragment "A" was treated with restriction enzymes BamHI and KpnI and the resulting fragment was inserted into BglIII/KpnI cut pTripb (Example 1) to obtain the vector pTH6FXscFv(CEA6)-tribp (Fig. 15) encoding the H6FXscFv(CEA6)-  
20 TRIPB fusion protein (Fig. 16). PCR fragment "B" was treated with restriction enzymes BamHI and HindIII and the resulting fragment was inserted into BamHI and HindIII cut pTripb (Example 1) to obtain the vector pTH6FXtribp-scFv(CEA6) (Fig. 17) encoding the H6FXTRIPB-scFv(CEA6) fusion protein (Fig. 18,  
25 SEQ ID NO: 33) using standard procedures.

- To generate the expression vector pTH6FXscFv(CEA6)-tribp-scFv(CEA6) (Fig. 19) encoding the H6FXscFv(CEA6)-TRIPB-scFv(CEA6) fusion protein (Fig. 20, SEQ ID NO: 34) the insert in the vector pTH6FXtribp-scFv(CEA6) was excised using re-  
30 striction enzymes BamHI and HindIII and inserted into the vector pTH6FXscFv(CEA6)-tribp, which had been treated with restriction enzymes BamHI and HindIII.

To prepare the chimeric fusion proteins H6FXscFv(CEA6)-TRIPB (SEQ ID NO: 32), H6FXTRIPB-scFv(CEA6) (SEQ ID NO: 33) and H6FXscFv(CEA6)-TRIPB-scFv(CEA6) (SEQ ID NO: 34) the plasmids pTH6FXscFv(CEA6)-TRIPB, pTH6FXtripb-scFv(CEA6) and pTH6FXscFv(CEA6)-tripb-scFv(CEA6) were grown in small scale (1 litre; 2xTY medium, 5 mM MgSO<sub>4</sub> and 100 µg ampicillin) in *E. coli* BL21 cells, as described by Studier et al. (1990). Exponentially growing cultures at 37°C were at OD<sub>600</sub> 0.8 infected with bacteriophage lambda CE6 at a multiplicity of approximately 5. Cultures were grown at 37°C for another three hours and the cells harvested by centrifugation. Cells were resuspended in 50 ml of 0.5 M NaCl, 50 mM Tris-HCl pH 8, and 1 mM EDTA pH 8. Phenol (50 ml adjusted to pH 8) was added to each and the mixtures were sonicated to extract total protein. After clarification by centrifugation (25 minutes at 10.000 g) crude protein fractions were precipitated from the phenol phases by addition of 2.5 volumes of ethanol and centrifugation. Protein pellets were dissolved in a buffer (15-25 ml) containing 6 M guanidinium chloride, 50 mM Tris-HCl pH 8 and 0.1 M dithioerythriol. Following gel filtration on Sephadex G-25 (Pharmacia, Sweden) into 8 M Urea, 1 M NaCl, 50 mM Tris-HCl pH 8 and 10 mM 2-mercaptoethanol, the crude protein preparations were applied to Ni<sup>2+</sup> activated NTA-agarose columns (75 ml column volume) for purification (Hochuli et al., 1988). Washing buffer (6 M guanidine-HCl, 50 mM Tris-HCl pH 8 and 10 mM 2-mercaptoethanol) was then flowed through the columns until stable baselines were obtained. Virtually pure fusion proteins could then be eluted by applying a pH gradient to each column (1000 ml gradient in 8 M urea and 10 mM 2-mercaptoethanol obtained by linear (per volume) mixing of solutions containing 50 mM sodium di-hydrogenphosphate (pH 5 buffer) and 50 mM di-sodium hydrogenphosphate (pH 8 buffer)).

In preparation for in vitro refolding by the method of Thøgersen et al. (WO 94/18227) 20 mg of each purified fusion protein were mixed in suspensions in refolding "buffer B" (described below) with aliquots of suspensions of Ni<sup>2+</sup> acti-

vated NTA-agarose matrix sufficient to generate columns of about 75 ml packed bed volume. Each fusion protein was then subjected to the iterative refolding procedure as described for plasminogen kringle 4 in the Thøgersen et al. patent application (WO 94/18227), except that refolding of the scFv containing fusion proteins was carried out at 10°C using a buffer containing 0.5 M NaCl, 50 mM Tris-HCl pH 8, 2 mM glutathione and 0.2 mM oxidized glutathione as "buffer A" and a buffer containing 8 M urea, 1 M NaCl, 50 mM Tris-HCl pH 8 and 2 mM glutathione as "buffer B".

After completion of the refolding procedure each column was washed with 300 ml buffer containing 0.5 M NaCl and 50 mM Tris-HCl pH 8 to wash away glutathione. The refolded fraction of each protein was then eluted from the NTA-agarose matrix by addition of 20 mM EDTA to the elution buffer. After addition of solid urea to achieve a final concentration of about 8 M to each protein sample and dilution or dialysis to reduce NaCl concentrations to below 5 mM, final purification of each correctly folded fusion protein product was then accomplished by ion exchange chromatography (S-Sepharose, Pharmacia, 1,6 (i.d.) by 90 centimeter column in a buffer containing 8 M urea, 5 mM Tris-HCl (from 1 M stock solution at pH 8) and 25 mM sodium acetate (from 1 M stock solution at pH 5), eluted at 2 ml/min). After dialysis against aqueous buffers (e.g. phosphate buffered saline) each pure and correctly refolded fusion protein was recovered in yields of 2-6 mg per litre of culture grown. Each protein may be shown by analytical gel filtration, chemical cross-linking analysis, by in vitro affinity measurements and by in vivo efficacy to form a stable homotrimeric molecular complex: The oligomeric status of the H6FXtripb-scFv-(CEA6) fusion protein was analyzed by chemical cross-linking analysis with DMSI: In parallel experiments, samples of H6FXtripb-scFv-(CEA6) at 0.34 mg/ml and TN123 at 0.28 mg/ml in 0.1 M Sodium borate were incubated at room temperature with increasing amounts (0 - 40 µg in 12 µl in total) of DMSI for 30 min. Reactions were quenched by addition of 5 µl 3M Tris-HCl pH 9 and the samples analyzed by

SDS-PAGE under reducing conditions (Fig. 21). Like tetranectin, the H6FXtripb-scFV-(CEA6) fusion protein, of approximately 38 kDa, is hereby shown to be a trimer in solution.

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## SEQUENCE LISTING

## (1) GENERAL INFORMATION

## (i) APPLICANT

- (A) NAME: Thøgersen, Hans Christian
- (B) STREET: Ristrupvej 41
- (C) CITY: Mundelstrup
- (D) STATE OR PROVINCE:
- (E) COUNTRY: Denmark
- (F) POSTAL CODE: 8381

(ii) TITLE OF THE INVENTION: Trimerising module

(iii) NUMBER OF SEQUENCES: 34

## (iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

## (v) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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47

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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33

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gly Ser Ile Gln Gly Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Val | Asn | Thr | Lys | Met | Phe | Glu | Glu | Leu | Lys | Ser | Arg | Leu | Asp | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ala | Gln | Glu | Val | Ala | Leu | Leu | Lys | Glu | Gln | Gln | Ala | Leu | Gln | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Ser | Leu | Lys |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

50

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | Pro | Thr | Gln | Lys | Pro | Lys | Lys | Ile | Val | Asn | Ala | Lys | Lys | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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      20          25          30
Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr
      35          40          45
Val

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## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp
 1          5          10          15
Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr
      20          25          30
Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr
      35          40          45
Val Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe
 50          55          60
Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp Cys Ile Ser Arg
 65          70          75          80
Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu
      85          90          95
Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu
      100          105          110
Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly
      115          120          125
Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro
      130          135          140
Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn
      145          150          155          160
Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys
      165          170          175
Gln Phe Gly Ile Val
      180

```

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCTGGATCCA TCGAGGGTAG GGGCGAGCCA CCAACCCAG

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCGAAGCTTA CACGATCCCG AACTG

25

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Ser Ile Glu Gly Arg  
1 5

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Val Arg Ala Asn Lys Arg Asn Glu Ala Leu Arg Ile Glu Ser Ala  
1 5 10 15  
Leu Leu Asn Lys Ile Ala Met Leu Gly Thr Glu Lys Thr Ala Glu Gly  
20 25 30

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Ser His His His His His Gly Ser  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCGAAGCTTA GACCGTCTGC AGGGC

25

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCGGATCCA TCCAGGGTAG GGTGTGAAC ACAAAGATG

39

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTGGATCCA TCGAGGGTAG GGCCCTGCAG ACGGTC

36

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGCAGATCT TTGTGAAGAC CCTCACTGGC AAAACCATCA CCCTTGAGGT CGAGCCCCAGT 60  
 GACACCATTG AGAATGTCAA AGCCAAAATT CAAGACAAGG AGGGTATCCC ACCTGACCGC 120  
 AGCGTCTGAT ATTTGCCGGC AAACAGCTGG AAGATGGACG TACTTTGTCT GACTACAATA 180  
 TTCAAAGGA GTCTACTCTT CATCTTGTGT TGAGACTTCG TGGTGGT 227

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGCTGATCAC AGATCTTTGT GAAGACC

27

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGCAAGCTTG CATGCTTAGG ATCCACCACG AAGTCTCAA

39

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Ile | Phe | Val | Lys | Thr | Leu | Thr | Gly | Lys | Thr | Ile | Thr | Leu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Glu | Pro | Ser | Asp | Thr | Ile | Glu | Asn | Val | Lys | Ala | Lys | Ile | Gln | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Lys | Glu | Gly | Ile | Pro | Pro | Asp | Gln | Arg | Leu | Ile | Phe | Ala | Gly | Lys |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Gln | Leu | Glu | Asp | Gly | Arg | Thr | Leu | Ser | Asp | Tyr | Asn | Ile | Gln | Lys | Glu |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Thr | Leu | His | Leu | Val | Leu | Arg | Leu | Arg | Gly | Gly |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGGTTTCAGC TGCAGCAGTC AGGGGCTGAG GTGAAGAAGC CTGGGTCTCTC GGTGAAGGTC

60

|            |            |            |             |            |             |     |
|------------|------------|------------|-------------|------------|-------------|-----|
| TCCTGCAAGG | CTTCTGGAGG | CACCTTCAGC | AACTCTCCTA  | TCAACTGGCT | GCGACAGGCC  | 120 |
| CCCGGACAAG | GGCTTGAGTG | GATGGGAAGT | ATCATCCCTT  | CCTTTGGTAC | AGCAAACCTAC | 180 |
| GCTCAGAAGT | TCCAGGGCAG | ACTCACGATT | ACCGCGGACG  | AATCCACGAG | CACAGCCTAC  | 240 |
| ATGGAGCTGA | GCAGCCTGAG | ATCTGAGGAC | ACGGCCGTGT  | ATTACTGTGC | GGGGCGGAGC  | 300 |
| CACAACTACG | AACTCTACTA | TTACTACATG | GACGTCTGGG  | GCCAGGGGAC | AATGGTCACC  | 360 |
| GTCTCGAGTG | GTGGAGGCGG | TTCAGGCGGA | GGTGGCAGCG  | GCGGTGGCGG | ATCGGACATC  | 420 |
| CAGATGACCC | AGTCTCCTTC | CACCCTGTCT | GCATCTATTG  | GAGACAGAGT | CACCATCACC  | 480 |
| TGCCGGGCCA | GTGAGGGTAT | TTATCACTGG | TTGGCCTGGT  | ATCAGCAGAA | GCCAGGGAAA  | 540 |
| CCCCCTAAAC | TCCTGATCTA | TAAGGCCTCT | AGTTTAGCCA  | GTGGGGCCCC | ATCAAGGTTC  | 600 |
| AGCGGCAGTG | GATCTGGGAC | AGATTTCACT | CTCACCATCA  | GCAGCCTGCA | GCCTGATGAT  | 660 |
| TTTGCAACTT | ATTACTGCCA | ACAATATAGT | AATTATCCGC  | TCACTTTCGG | CGGAGGGACC  | 720 |
| AAGCTGGAGA | TCAAACGTGC | GGCCGCAGAA | CAAAAACCTCA | TCTCAGAAGA | GGATCTGAAT  | 780 |
| GGGGCC     |            |            |             |            |             | 786 |

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGTGGATCCC AGGTTTCAGCT GCAGC 25

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCGGTACCG GCCCATTCA GATCC 25

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCCAAGCTTA GGCCCCATTC AGATCC 26

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid



(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Met Val Arg Ala Asn Lys Arg Asn Glu Ala Leu Arg Ile Glu Ser Ala
 1           5           10           15
Leu Leu Asn Lys Ile Ala Met Leu Gly Thr Glu Lys Thr Ala Glu Gly
      20           25           30
Gly Ser His His His His His Gly Ser Ile Glu Gly Arg Gly Glu
      35           40           45
Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val
      50           55           60
Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu
      65           70           75           80
Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val
      85           90           95
Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr
      100          105          110
Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp Cys Ile Ser Arg Gly
      115          120          125
Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr
      130          135          140
Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly
      145          150          155          160
Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala
      165          170          175
Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
      180          185          190
Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
      195          200          205
Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
      210          215          220
Phe Gly Ile Val
      225

```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Met Gly Ser His His His His His His Gly Ser Ile Glu Gly Arg Gly
 1           5           10           15
Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp
      20           25           30
Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr
      35           40           45
Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr
      50           55           60

```

```

Val Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe
65          70          75          80
Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp Cys Ile Ser Arg
          85          90          95
Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu
          100          105          110
Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu
          115          120          125
Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly
          130          135          140
Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro
145          150          155          160
Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn
          165          170          175
Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys
          180          185          190
Gln-Phe Gly Ile Val
          195

```

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Met Gly Ser His His His His His His Gly Ser Ile Glu Gly Arg Gly
1          5          10          15
Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp
          20          25          30
Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr
          35          40          45
Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr
          50          55          60
Val
65

```

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Val
1          5          10          15
Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu
          20          25          30

```

Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val  
 35 40 45  
 Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr  
 50 55 60  
 Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp Cys Ile Ser Arg Gly  
 65 70 75 80  
 Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr  
 85 90 95  
 Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly  
 100 105 110  
 Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala  
 115 120 125  
 Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp  
 130 135 140  
 Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly  
 145 150 155 160  
 Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln  
 165 170 175  
 Phe Gly Ile Val  
 180

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Ser  
 1 5 10 15  
 Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala  
 20 25 30  
 Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg  
 35 40 45  
 Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala  
 50 55 60  
 Leu Gln Thr Val Ser Leu Lys Gly Ser  
 65 70

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Ser  
 1 5 10 15

Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala  
                   20                  25                  30  
 Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg  
           35                  40                  45  
 Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala  
       50                  55                  60  
 Leu Gln Thr Gly Ser  
 65

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Gly Ser His His His His His His Gly Ser Ile Glu Gly Arg Ala  
   1                  5                  10                  15  
 Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe  
           20                  25                  30  
 Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp Cys  
       35                  40                  45  
 Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn  
       50                  55                  60  
 Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu  
   65                  70                  75                  80  
 Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp  
           85                  90                  95  
 Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr  
          100                 105                 110  
 Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly  
       115                 120                 125  
 Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro  
      130                 135                 140  
 Tyr Ile Cys Gln Phe Gly Ile Val  
 145                 150

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Ser  
   1                  5                  10                  15  
 Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala  
           20                  25                  30

```

Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg
  35              40              45
Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala
  50              55              60
Leu Gln Thr Gly Ser Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr
  65              70              75              80
Ile Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala
              85              90              95
Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile
              100              105              110
Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn
              115              120              125
Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly
              130              135              140
Ser
145

```

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Ser
  1              5              10              15
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
              20              25              30
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Ser
              35              40              45
Pro Ile Asn Trp Leu Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
              50              55              60
Gly Ser Ile Ile Pro Ser Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
              65              70              75              80
Gln Gly Arg Leu Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
              85              90              95
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
              100              105              110
Ala Gly Arg Ser His Asn Tyr Glu Leu Tyr Tyr Tyr Tyr Met Asp Val
              115              120              125
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
              130              135              140
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
              145              150              155              160
Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr
              165              170              175
Cys Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln
              180              185              190
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu
              195              200              205
Ala Ser Gly Ala Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
              210              215              220

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Pro | Asp | Asp | Phe | Ala | Thr | Tyr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Tyr | Cys | Gln | Gln | Tyr | Ser | Asn | Tyr | Pro | Leu | Thr | Phe | Gly | Gly | Gly | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Leu | Glu | Ile | Lys | Arg | Ala | Ala | Ala | Glu | Gln | Lys | Leu | Ile | Ser | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Asp | Leu | Asn | Gly | Ala | Gly | Thr | Glu | Pro | Pro | Thr | Gln | Lys | Pro | Lys |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Ile | Val | Asn | Ala | Lys | Lys | Asp | Val | Val | Asn | Thr | Lys | Met | Phe | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Leu | Lys | Ser | Arg | Leu | Asp | Thr | Leu | Ala | Gln | Glu | Val | Ala | Leu | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Glu | Gln | Gln | Ala | Leu | Gln | Thr | Gly | Ser |     |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | His | His | His | His | His | His | Gly | Ser | Ile | Gln | Gly | Arg | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Gly | Thr | Glu | Pro | Pro | Thr | Gln | Lys | Pro | Lys | Lys | Ile | Val | Asn | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Lys | Asp | Val | Val | Asn | Thr | Lys | Met | Phe | Glu | Glu | Leu | Lys | Ser | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Asp | Thr | Leu | Ala | Gln | Glu | Val | Ala | Leu | Leu | Lys | Glu | Gln | Gln | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Gln | Thr | Gly | Ser | Gln | Val | Gln | Leu | Gln | Gln | Ser | Gly | Ala | Glu | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Lys | Pro | Gly | Ser | Ser | Val | Lys | Val | Ser | Cys | Lys | Ala | Ser | Gly | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Ser | Asn | Ser | Pro | Ile | Asn | Trp | Leu | Arg | Gln | Ala | Pro | Gly | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Leu | Glu | Trp | Met | Gly | Ser | Ile | Ile | Pro | Ser | Phe | Gly | Thr | Ala | Asn |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Ala | Gln | Lys | Phe | Gln | Gly | Arg | Leu | Thr | Ile | Thr | Ala | Asp | Glu | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Ser | Thr | Ala | Tyr | Met | Glu | Leu | Ser | Ser | Leu | Arg | Ser | Glu | Asp | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Val | Tyr | Tyr | Cys | Ala | Gly | Arg | Ser | His | Asn | Tyr | Glu | Leu | Tyr | Tyr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Tyr | Met | Asp | Val | Trp | Gly | Gln | Gly | Thr | Met | Val | Thr | Val | Ser | Ser |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Asp |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Thr | Leu | Ser | Ala | Ser | Ile | Gly | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Val | Thr | Ile | Thr | Cys | Arg | Ala | Ser | Glu | Gly | Ile | Tyr | His | Trp | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Ala | Ser | Ser | Leu | Ala | Ser | Gly | Ala | Pro | Ser | Arg | Phe | Ser | Gly | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Pro | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Tyr | Ser | Asn | Tyr | Pro | Leu | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Phe | Gly | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Ala | Ala | Ala | Glu | Gln |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Leu | Ile | Ser | Glu | Glu | Asp | Leu | Asn | Gly | Ala |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | His | His | His | His | His | His | Gly | Ser | Ile | Gln | Gly | Arg | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Val | Gln | Leu | Gln | Gln | Ser | Gly | Ala | Glu | Val | Lys | Lys | Pro | Gly | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Val | Lys | Val | Ser | Cys | Lys | Ala | Ser | Gly | Gly | Thr | Phe | Ser | Asn | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Ile | Asn | Trp | Leu | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu | Glu | Trp | Met |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Ser | Ile | Ile | Pro | Ser | Phe | Gly | Thr | Ala | Asn | Tyr | Ala | Gln | Lys | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Gly | Arg | Leu | Thr | Ile | Thr | Ala | Asp | Glu | Ser | Thr | Ser | Thr | Ala | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Glu | Leu | Ser | Ser | Leu | Arg | Ser | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Gly | Arg | Ser | His | Asn | Tyr | Glu | Leu | Tyr | Tyr | Tyr | Tyr | Met | Asp | Val |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Trp | Gly | Gln | Gly | Thr | Met | Val | Thr | Val | Ser | Ser | Gly | Gly | Gly | Gly | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser | Asp | Ile | Gln | Met | Thr | Gln |     |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ser | Pro | Ser | Thr | Leu | Ser | Ala | Ser | Ile | Gly | Asp | Arg | Val | Thr | Ile | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Cys | Arg | Ala | Ser | Glu | Gly | Ile | Tyr | His | Trp | Leu | Ala | Trp | Tyr | Gln | Gln |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile | Tyr | Lys | Ala | Ser | Ser | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Ser | Gly | Ala | Pro | Ser | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Pro | Asp | Asp | Phe | Ala | Thr | Tyr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Tyr | Cys | Gln | Gln | Tyr | Ser | Asn | Tyr | Pro | Leu | Thr | Phe | Gly | Gly | Gly | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |

Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu  
 260 265 270  
 Glu Asp Leu Asn Gly Ala Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys  
 275 280 285  
 Lys Ile Val Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu  
 290 295 300  
 Glu Leu Lys Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu  
 305 310 315 320  
 Lys Glu Gln Gln Ala Leu Gln Thr Gly Ser Gln Val Gln Leu Gln Gln  
 325 330 335  
 Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys  
 340 345 350  
 Lys Ala Ser Gly Gly Thr Phe Ser Asn Ser Pro Ile Asn Trp Leu Arg  
 355 360 365  
 Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Ser Ile Ile Pro Ser  
 370 375 380  
 Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Leu Thr Ile  
 385 390 395 400  
 Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu  
 405 410 415  
 Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Gly Arg Ser His Asn  
 420 425 430  
 Tyr Glu Leu Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Gln Gly Thr Met  
 435 440 445  
 Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly  
 450 455 460  
 Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser  
 465 470 475 480  
 Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly  
 485 490 495  
 Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro  
 500 505 510  
 Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser  
 515 520 525  
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
 530 535 540  
 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser  
 545 550 555 560  
 Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg  
 565 570 575  
 Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala  
 580 585 590



## CLAIMS

1. A monomer polypeptide construct comprising at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, said TTSE being  
5 capable of forming a stable triple alpha helical coiled coil complex with two other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins C11H6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23, the sequences of which are shown in SEQ ID NOs: 24-27.
2. A monomer polypeptide construct comprising at least one tetranectin trimerising structural  
10 element (TTSE) which is covalently linked to at least one heterologous moiety, said TTSE being capable of forming a stable triple alpha helical coiled coil complex with two other TTSEs, said at least one heterologous moiety being one which does not exclusively facilitate expression and/or purification of the monomer polypeptide construct.
- 15 3. A monomer polypeptide construct according to any of the preceding claims, wherein the heterologous moiety is selected from the group consisting of a ligand binding structure; a toxin; a detectable label; an in situ activatable substance; an enzyme; a radioactive moiety; a cytokine; a non-proteinaceous polymer such as a polymeric alkaloid, a polyalcohol, a polysaccharide, a lipid and a polyamine; a photo cross-linking agent; and a group facilitating conjugation of the monomer  
20 polypeptide construct to a target.
4. A monomer polypeptide construct according to any of the preceding claims, which comprises 2 TTSEs which are covalently linked by a spacer moiety which allows both of the 2 TTSEs to take part in complex formation with a third TTSE not being part of the monomer polypeptide construct.  
25
5. A monomer polypeptide construct according to claim 4, wherein the spacer moiety has a length and a conformation which favours complex formation involving both of the two TTSEs which are covalently linked by the spacer moiety.
- 30 6. A monomer polypeptide construct according to claim 4 or 5, wherein the spacer moiety is a polypeptide fragment.
7. A monomer polypeptide construct according to any of claims 1-3, which comprises one single TTSE.

8. A monomer polypeptide construct according to any of the preceding claims, wherein the TTSE is derived from human tetranectin, murine tetranectin, C-type lectin of bovine cartilage, or C-type lectin of shark cartilage.
- 5 9. A monomer polypeptide construct according to claim 8, wherein the TTSE comprises a polypeptide sequence which has at least 68% sequence identity with the consensus sequence shown in Fig. 2.
- 10 10. A monomer polypeptide construct according to claim 9, wherein the sequence identity with the consensus sequence is at least 75%, such as at least 81%, at least 87%, or at least 92%.
11. A monomer polypeptide construct according to any of claims 8-10, wherein at least one amino acid residue selected from the group consisting of amino acid residue nos. 6, 21, 22, 24, 25, 27, 28, 31, 32, 35, 39, 41, 42, is/are substituted by any non-helix breaking amino acid residue, the amino  
15 acid residue numbering referring to amino acid residues in SEQ ID NO: 7.
12. A monomer polypeptide construct according to any of the preceding claims, wherein the at least one TTSE comprises a repeated heptad having the formula a-b-c-d-e-f-g (N to C), wherein a majority of the amino acids residues a and d are hydrophobic amino acids.
- 20 13. A monomer polypeptide construct according to claim 12, wherein heptad is repeated 3 times and wherein the last occurrence of the heptad has a glutamine residue corresponding to residues a and d.
14. A monomer polypeptide construct according to any of the preceding claims, wherein the at least  
25 one heterologous moiety is covalently linked to the TTSE via a peptide bond to the N- or C-terminus of the TTSE peptide chain, via a peptide bond to a side chain in the TTSE, via a bond to a cysteine residue, or when more than one heterologous moiety, combinations of these locations.
15. A monomer polypeptide construct according to any of the preceding claims which lacks any free  
30 amino and/or carboxy groups.
16. A monomer polypeptide construct according to any of the preceding claims which lacks a substantial part of the N-terminal region of tetranectin which is encoded by exon 1.

17. A monomer polypeptide construct according to any of the preceding claims comprising two heterologous moieties which are linked via peptide bonds to the N- and C-terminus, respectively.

18. A monomer polypeptide construct according to any of the preceding claims which is constructed  
5 so as to disfavour formation of complexes between identical TTSEs.

19. An oligomer which is comprised of two monomer polypeptide constructs according to any of claims 1-18, and which comprises at least three TTSE's or a multipum of three TTSE's, or which is comprised of three monomer polypeptide constructs according to any of claims 1-3 or 7-18.

10

20. An oligomer according to claim 19 which is stable in the temperature range 50-70°C.

21. An oligomer according to claim 19 or 20, which comprises at least one heterologous moiety which is positioned N-terminally to a TTSE and at least one heterologous moiety which is  
15 positioned C-terminally to a TTSE.

22. An oligomer according to claim 21, wherein the at least one heterologous moiety which is positioned N-terminally to a TTSE and the at least one heterologous moiety which is positioned C-terminally to a TTSE are part of the same monomeric polypeptide construct.

20

23. An oligomer according to claim 21, wherein the at least one heterologous moiety which is positioned N-terminally to a TTSE and the at least one heterologous moiety which is positioned C-terminally to a TTSE are part of two separate monomeric polypeptide constructs.

24. An oligomer according to any of claims 19-23, wherein each monomer polypeptide construct is designed so as to disfavour formation of trimers including two monomer polypeptide constructs having identical TTSEs.

25. A method of preparing a monomer polypeptide construct according to any of claims 1-18, the  
30 method comprising

- isolating the monomer polypeptide construct from a culture comprising a host cell which carries and expresses a nucleic acid fragment which encodes the monomer polypeptide construct, or

35

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- synthesizing, by means of chemical peptide synthesis, the monomer polypeptide construct and subsequently isolating the monomer polypeptide construct from the reaction mixture, or
- preparing a TTSE in a culture comprising a host cell which carries and expresses a nucleic acid fragment which encodes the TTSE, subsequently linking covalently at least one  
5 heterologous moiety to the TTSE, and thereafter isolating the resulting monomer polypeptide construct, or
- synthesizing, by means of chemical peptide synthesis, a TTSE, subsequently linking  
10 covalently at least one heterologous moiety to the TTSE, and thereafter the isolating the resulting monomer polypeptide construct from the reaction mixture,

and optionally subjecting the monomer polypeptide construct to further processing.

15 26. A method for preparing a dimeric oligomer according to claim 19 which comprises

- admixing a monomer polypeptide construct according to any of claims 1-18 which includes two TTSEs (construct 1) with a monomer polypeptide construct according to any of claims 1-3 or 7-18 which includes only one TTSE (construct 2),  
20
- effecting the two TTSE's of construct 1 to complex with the TTSE of construct 2, and
- isolating the resulting dimer and optionally subjecting the dimer to further processing.

25 27. A method for preparing a trimeric oligomer according to claim 19 which comprises

- admixing three monomer polypeptide constructs according to any of claims 1-18 with each other,  
30
- effecting complex formation between one TTSE of each monomer polypeptide construct, and
- isolating the resulting trimer and optionally subjecting the trimeric oligomer to further processing.

35 28. A kit comprising

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5

- a first package comprising at least one container means, each at least one container means containing a monomer polypeptide construct according to any of claims 1-18,
- 5 - a second package comprising at least one container means, each at least one container means in the second package containing a monomer polypeptide construct according to any of claims 1-18, the second package being different from the first package with respect to choice and/or number of monomer polypeptide constructs included therein, and optionally
- 10 - a third package comprising at least one container means, each at least one container means in the third package containing a monomer polypeptide construct according to any of claims 1-18, the second package being different from the first and second packages with respect to choice and/or number of monomer polypeptide constructs included therein.
- 15 29. A kit according to claim 28, wherein the at least one container means in each package contains mutually distinct monomer polypeptide constructs.
- 30. A kit according to claim 28 or 29, wherein all container means comprised in the kit comprises mutually distinct polypeptide constructs.
- 20 31. A nucleic acid fragment in isolated form which encodes a TTSE as defined in any of claims 1-18 or which encodes the polypeptide part of a monomer polypeptide construct according to any of claims 1-18, with the proviso that the nucleic acid fragment is different from one that encodes native members of the tetranectin family, and that the nucleic acid fragment is different from one that
- 25 encodes any of the fusion proteins C11H6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23, the sequences of which are shown in SEQ ID NOs: 24-27.
- 32. A replicable vector which comprises a nucleic acid fragment according to claim 31.
- 30 33. A transformed host cell, which comprises a nucleic acid fragment according to claim 31 or a replicable vector according to claim 31.
- 34. Use of a monomer polypeptide construct according to any of claims 1-18 or to a an oligomer construct according to any of claims 19-24 for targeted gene therapy involving selective delivery of
- 35 the material for transfection or infection of the specific population of cells.

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35. The use according to claim 34 wherein the at least one heterologous moiety comprises a moiety selected from a ligand binding structure such as a receptor molecule or the ligand binding part of a receptor molecule, and wherein the gene therapy involves the delivery of nucleic acids to the desired population of cells by use of a viral vector directed to cells displaying the artificial receptor complex corresponding to the heterologous moiety.

36. The use of a monomer polypeptide construct according to any of claims 1-18 or to a an oligomer according to any of claims 19-24 as a component of a chimaeric product having low antigenicity in humans relative to formulations comprising on or more components of non-human origin.

37. The use of a monomer polypeptide construct according to any of claims 1-18 or to a an oligomer according to any of claims 19-24 as a vehicle for assembling antibody fragments into oligomeric or multivalent entities for generating chimeric artificial antibodies having preselected pharmacokinetic and/or pharmacodynamic properties.

38. The use of a monomer polypeptide construct according to any of claims 1-18 or to a an oligomer according to any of claims 19-24 for delivering an imaging or toxin-conjugated antibody to a tumor.

39. The use of a monomer polypeptide construct according to any of claims 1-18 or to a oligomer according to any of claims 19-24 as a vehicle delivering an substance to a target cell or tissue.

40. The use of a monomer polypeptide construct according to any of claims 1-18 or to a oligomer according to any of claims 19-24 for a labelled construct wherein the label is coupled to one or to of the TTSE monomer units.

41. The use of a monomer polypeptide construct according to any of claims 1-18 or to a oligomer according to any of claims 19-24 for protein library technology, such as phage display technology.

42. The use according to claim 41 comprising a poly nucleotide molecule encoding one or more TTSE.

43. The use according to claim 41 comprising a vector encoding one or more TTSE.

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44. The use of a monomer polypeptide construct according to any of claims 1-18 or to a oligomer according to any of claims 19-24 for the preparation of a pharmaceutical composition.

45. The use according to any to claim 44, wherein the pharmaceutical composition further comprises  
5 a pharmaceutically acceptable excipient.

46. The use according to claim 44 or 45 wherein the pharmaceutical composition is administered by a route selected from the group consisting of the intravenous route, the intraarterial route, the transmembraneus route of the buccal, anal, vaginal or conjunctival tissue, the intranasal route, the  
10 pulmonary route, the transdermal route, the intramuscular routed, subcutaneous route, intratechal route, inoculation into tissue such as a tumour, or by an implant.

47. The use according to any of claims 34 to 46  
wherein the monomer polypeptide construct according to any of claims 1-18 or the oligomer  
15 according to any of claims 19-24 is comprised in a liposome

48. A method for treating or preventing of a disease comprising administering to the subject in need thereof an effective amount of a pharmaceutical composition as defined in any of claims 44 and 45.

20 49. A method for treating or preventing a disease comprising administering to the subject in need thereof an effective amount of a relevant pharmaceutical coupled to a monomer polypeptide construct according to any of claims 1-18 or to a oligomer according to any of claims 19-24.

50. A method for targeted gene therapy comprising use of a monomer polypeptide construct  
25 according to any of claims 1-19 or to a oligomer according to any of claims 19-24.

51. A method of human gene therapy comprising use of a monomer polypeptide construct according to any of claims 1-18 or to an oligomer according to any of claims 19-24 wherein at least one TTSE is modified with a membrane integrating or associating entity having affinity to the specific  
30 population of cells in the body relevant for the gene therapy.

52. A method according to any of claims 48 to 51  
wherein the monomer polypeptide construct according to any of claims 1-18 or the oligomer according to any of claims 19-24 is administered by a route selected from the group consisting of the  
35 intravenous route, the intraarterial route, the transmembraneus route of the buccal, anal og vaginal

tissue, intranasal route, the pulmonary route, the transdermal route, intramuscular, subcutaneous, intratechal, the buccal, inoculation into tissue such as a tumour, or by an implant.

53. A method for prevention and/or treating a disease, comprising administering to a mammal in  
5 need thereof a prophylactically or therapeutically effective amount of a construct comprising the monomer polypeptide construct according to any of claims 1-18 or the oligomer according to any of claims 19-24.

54. A method for diagnosis comprising a construct comprising the monomer polypeptide construct  
10 according to any of claims 1-18 or the oligomer according to any of claims 19-24 together with a diagnosing component coupled thereon.



Exon 1

Trimer stabilising

Exon 2

Tripple alpha helical coiled coil  
forming

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E<sub>1</sub>P<sub>2</sub>P T Q K P K K I V N A K K D<sub>16</sub> V<sub>17</sub> V N T K M F E E L K S R L D T L A Q E V A L L K E Q Q A L Q T V C L<sub>51</sub>

Fig. 1

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| Position             | d | e | f | g | a | b | c | d | e | f | g | a |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|----------------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Human tetranectin    | V | V | N | T | K | M | F | E | E | L | K | S | R | L | D | T | L | A | Q | E | V | A | L | L | K | E | Q | A | L | Q | T | V | C | L | K |   |
| Murine tetranectin   | L | V | S | K | M | F | E | E | L | K | N | R | M | D | V | L | A | Q | E | V | A | L | L | K | E | K | Q | A | L | Q | T | V | C | L | K |   |
| Bovine cart. protein | R | R | V | K | E | K | D | G | D | L | K | T | Q | V | E | K | L | W | R | E | V | N | A | L | K | E | M | Q | A | L | Q | T | V | C | L | R |
| Shark cart. protein  | S | K | S | G | K | G | K | D | D | L | R | N | E | I | D | K | L | W | R | E | V | N | S | L | K | E | M | Q | A | L | Q | T | V | C | L | K |
| Consensus            | L |   |   |   |   |   |   |   |   |   | h | y |   |   | L |   | E | V |   |   |   |   |   | L | K | E | Q | A | L | Q | T | V | C | L |   |   |

Fig. 2

**tripa**

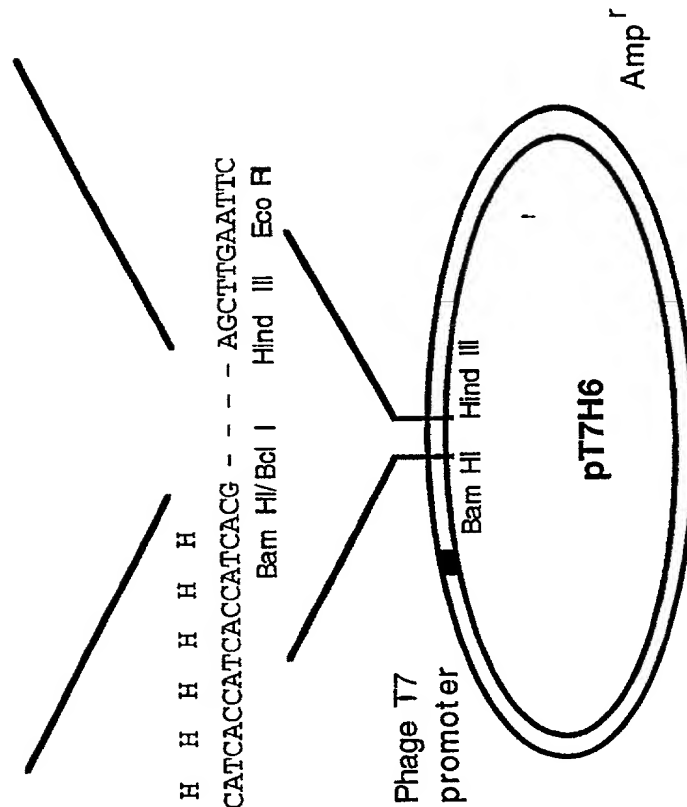
G S I Q G R S P G T E P P T T V S L K G S \*  
GATCAATCCAGGGAAGATCTCTGTGTTACCGAGCCACCAACC - - - - - ACGGTCTCCCTGAAGGATCCTAA  
Bcl II Kpn II Bam HI

**tripb**

G S I Q G R S P G T E P P T A L Q T G S \*  
GATCAATCCAGGGAAGATCTCTGGTACCGAGCCACCAACC ----- GCCCTGCAGACGGGATCCTAA  
Bgl II Kpn II Bam HI

M G S H H H H H

CATATGGGATCGCATCACCATCACCATCAG - - - AGCTTGAATTC  
Bam H/Bcl I Hind III Eco R



**Fig. 3**

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**H6FXtripa fusion protein**

1 M G S H H H H H H G S I Q G R S P G T E P P T Q K P K K I V 30  
31 N A K K D V V N T K M F E E L K S R L D T L A Q E V A L L K 60  
61 E Q Q A L Q T V S L K G S \* 73

**H6FXtripB fusion protein**

1 M G S H H H H H H G S I Q G R S P G T E P P T Q K P K K I V 30  
31 N A K K D V V N T K M F E E L K S R L D T L A Q E V A L L K 60  
61 E Q Q A L Q T G S \* 69

**Fig. 4**

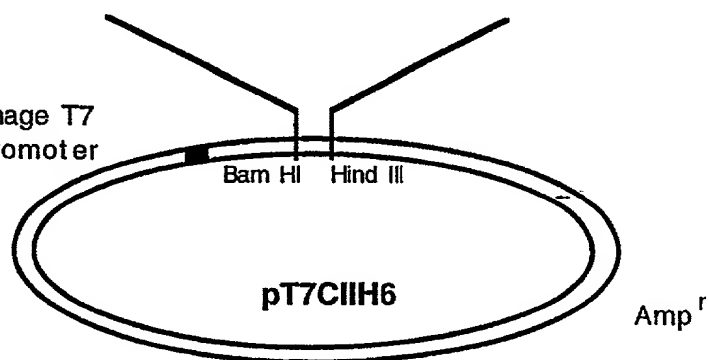
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TN123

G S I E G R G E P I V \*  
 GATCCATCGAGGGTAGGGGCGAGCCA --- ATCGTGTA

M V R A- **CII** -E G G S H H H H H  
 CATATGGTTCGTGCA -----GAAGGGGGATCGCATCACCATCACCATCAG - - - - AGCTTGAATTC  
Bam HI Hind III Eco RI

Phage T7  
promoter



TN123

G S I E G R G E P I V \*  
 GATCCATCGAGGGTAGGGGCGAGCCA --- ATCGTGTA

M G S H H H H H H  
 CATATGGGATCGCATCACCATCACCATCAG - - - - AGCTTGAATTC  
Bam HI Hind III Eco RI

Phage T7  
promoter

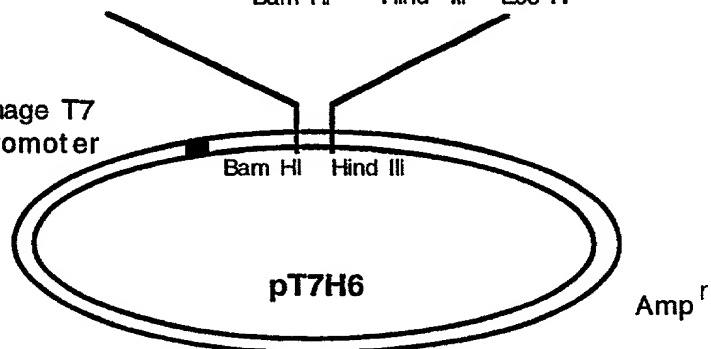


Fig. 5

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**CIH6FXTN123 fusion protein**

1 M V R A N K R N E A L R I E S A L L N K I A M L G T E K T A 30  
31 E G G S H H H H H H G S I E G R G E P P T Q K P K K I V N A 60  
61 K K D V V N T K M F E E L K S R L D T L A Q E V A L L K E Q 90  
91 Q A L Q T V C L K G T K V H M K C F L A F T Q T K T F H E A 120  
121 S E D C I S R G G T L S T P Q T G S E N D A L Y E Y L R Q S 150  
151 V G N E A E I W L G L N D M A A E G T W V D M T G A R I A Y 180  
181 K N W E T E I T A Q P D G G K T E N C A V L S G A A N G K W 210  
211 F D K R C R D Q L P Y I C Q F G I V \* 228

**H6FXTN123 fusion protein**

1 M G S H H H H H H G S I E G R G E P P T Q K P K K I V N A K 30  
31 K D V V N T K M F E E L K S R L D T L A Q E V A L L K E Q Q 60  
61 A L Q T V C L K G T K V H M K C F L A F T Q T K T F H E A S 90  
91 E D C I S R G G T L S T P Q T G S E N D A L Y E Y L R Q S V 120  
121 G N E A E I W L G L N D M A A E G T W V D M T G A R I A Y K 150  
151 N W E T E I T A Q P D G G K T E N C A V L S G A A N G K W F 180  
181 D K R C R D Q L P Y I C Q F G I V \* 197

**Fig. 6**

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**TN12**      G S I E G R G E P P      Q T V \*  
 GATCCATCGAGGGTAGGGGCGAGCCACCA ---- CAGACGGTCTA

**TN23**      G S I Q G R V V N T      G I V \*  
 GATCCATCCAGGGTAGGGTTGTGAACACA ---- GGGATCGTGTA

**TN3**      G S I E G R A L Q      G I V \*  
 GATCCATCGAGGGTAGGGCCCTGCAG ---- GGGATCGTGTA

M G S H H H H H H  
 CATATGGGATCGCATCACCATCACCATCACG - - - - AGCTTGAATTC  
                                  Bam HI    Hind III    Eco RI

Phage T7  
 promoter

Bam HI    Hind III

pT7H6

Amp<sup>r</sup>

Fig. 7

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**H6FXTN12 fusion protein**

```
1  M G S H H H H H H G S I E G R G E P P T Q K P K K I V N A K 30
31 K D V V N T K M F E E L K S R L D T L A Q E V A L L K E Q Q 60
61 A L Q T V * 65
```

**H6FXTN23 fusion protein**

```
1  M G S H H H H H H G S I Q G R V V N T K M F E E L K S R L D 30
31 T L A Q E V A L L K E Q Q A L Q T V C L K G T K V H M K C F 60
61 L A F T Q T K T F H E A S E D C I S R G G T L S T P Q T G S 90
91 E N D A L Y E Y L R Q S V G N E A E I W L G L N D M A A E G 120
121 T W V D M T G A R I A Y K N W E T E I T A Q P D G G K T E N 150
151 C A V L S G A A N G K W F D K R C R D Q L P Y I C Q F G I V 180
181 *
```

**H6FXTN3 fusion protein**

```
1  M G S H H H H H H G S I E G R A L Q T V C L K G T K V H M K 30
31 C F L A F T Q T K T F H E A S E D C I S R G G T L S T P Q T 60
61 G S E N D A L Y E Y L R Q S V G N E A E I W L G L N D M A A 90
91 E G T W V D M T G A R I A Y K N W E T E I T A Q P D G G K T 120
121 E N C A V L S G A A N G K W F D K R C R D Q L P Y I C Q F G 150
151 I V * 152
```

**Fig. 8**



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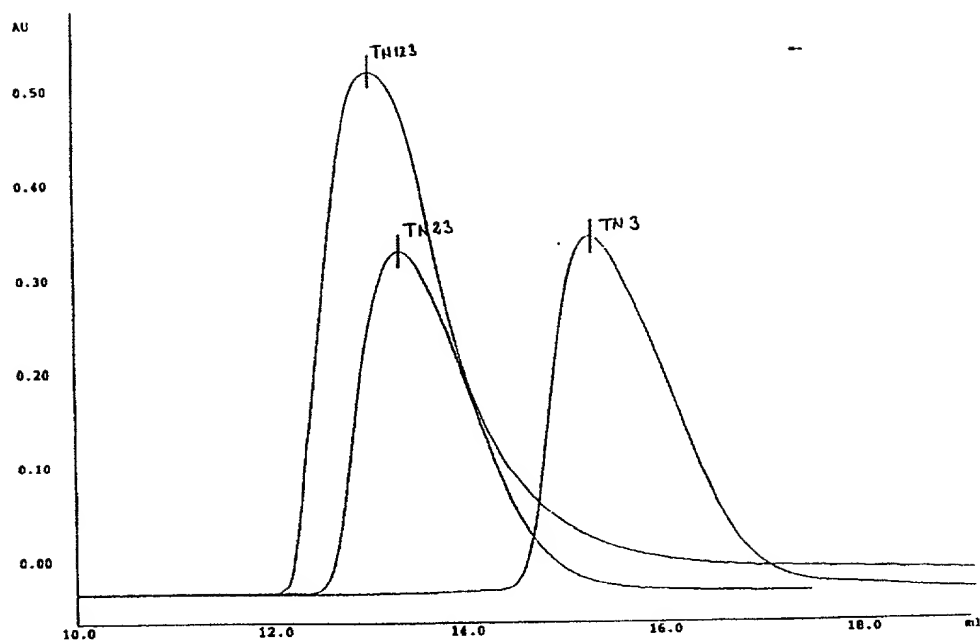


Fig. 9

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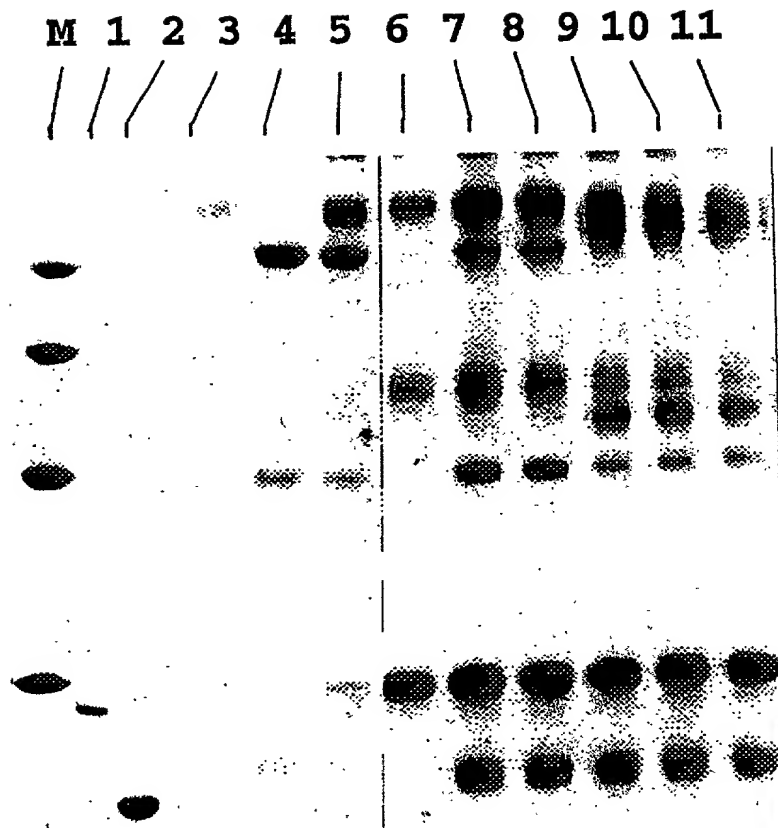


Fig. 10

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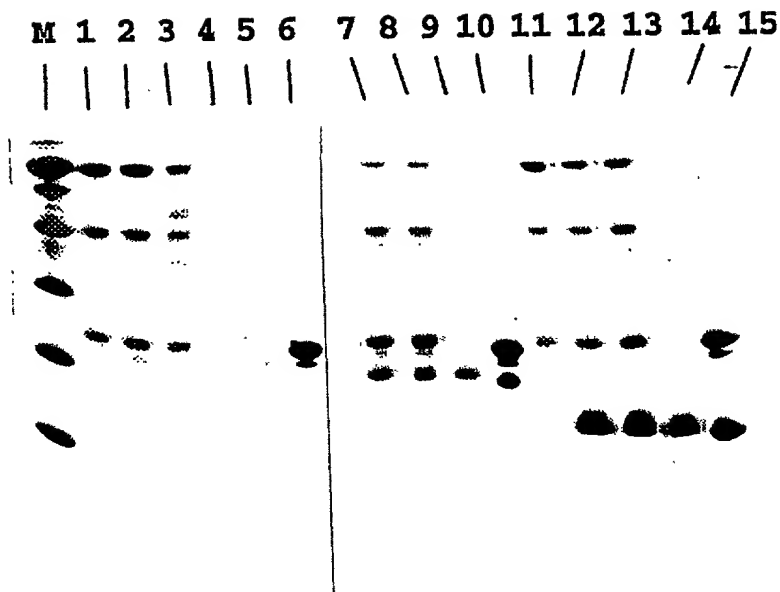


Fig. 11

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Fig. 12

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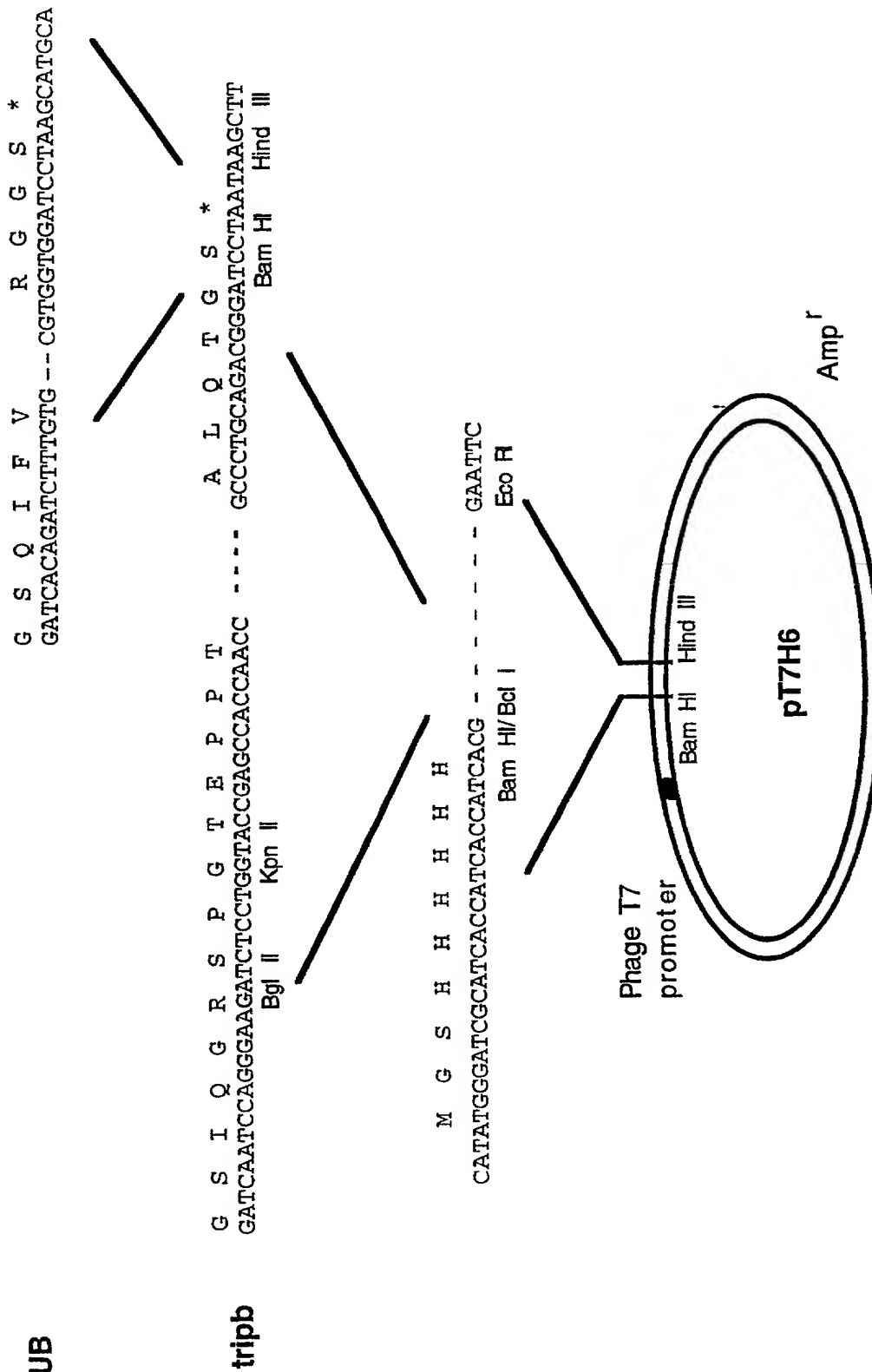


Fig. 13

Fig. 13

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**H6FXtripb-UB fusion protein**

1 M G S H H H H H H G S I Q G R S P G T E P P T Q K P K K I V 30  
31 N A K K D V V N T K M F E E L K S R L D T L A Q E V A L L K 60  
61 E Q Q A L Q T G S Q I F V K T L T G K T I T L E V E P S D T 90  
91 I E N V K A K I Q D K E G I P P D Q Q R L I F A G K Q L E D 120  
121 G R T L S D Y N I Q K E S T L H L V L R L R G G S \* 145

**Fig. 14**

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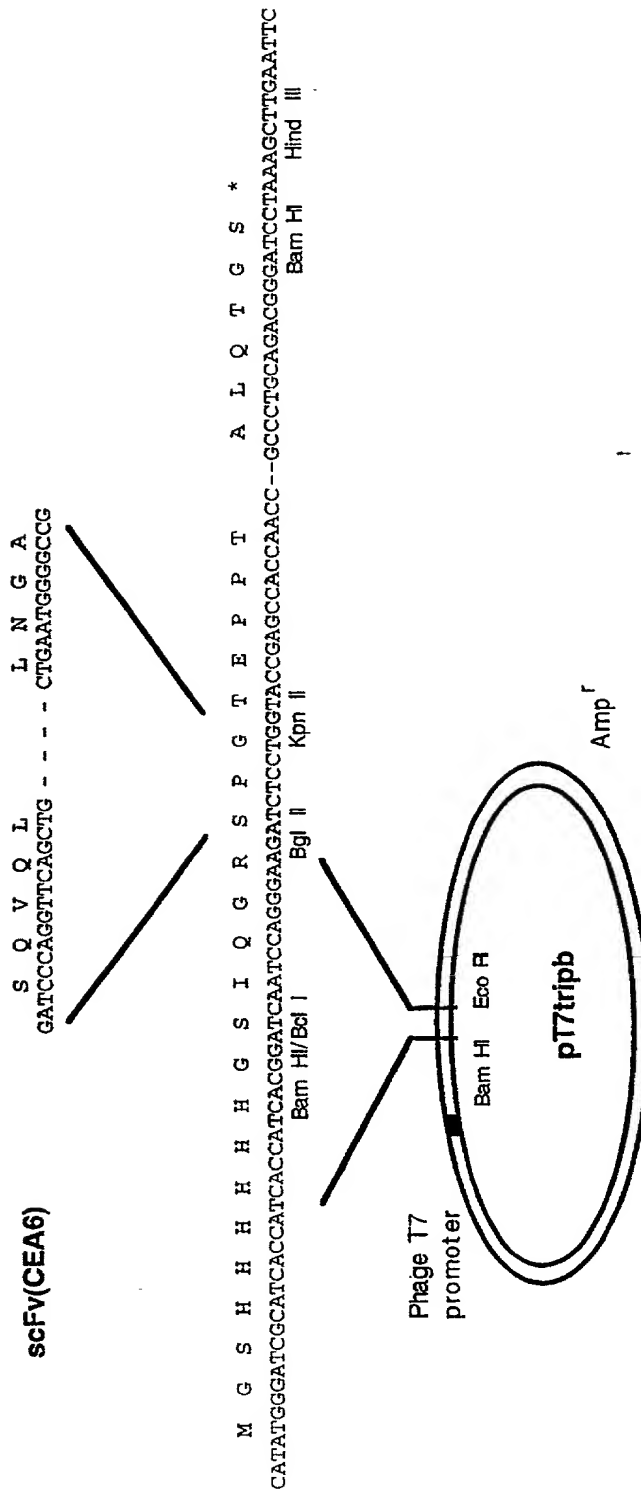


Fig. 15

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**H6FXscFv(CEA6)-triph fusion protein**

1 M G S H H H H H H G S I Q G R S Q V Q L Q Q S G A E V K K P 30  
31 G S S V K V S C K A S G G T F S N S P I N W L R Q A P G Q G 60  
61 L E W M G S I I P S F G T A N Y A Q K F Q G R L T I T A D E 90  
91 S T S T A Y M E L S S L R S E D T A V Y Y C A G R S H N Y E 120  
121 L Y Y Y Y M D V W G Q G T M V T V S S G G G G S G G G G S G 150  
151 G G G S D I Q M T Q S P S T L S A S I G D R V T I T C R A S 180  
181 E G I Y H W L A W Y Q Q K P G K A P K L L I Y K A S S L A S 210  
211 G A P S R F S G S G S G T D F T L T I S S L Q P D D F A T Y 240  
241 Y C Q Q Y S N Y P L T F G G G T K L E I K R A A A E Q K L I 270  
271 S E E D L N G A G T E P P T Q K P K K I V N A K K D V V N T 300  
301 K M F E E L K S R L D T L A Q E V A L L K E Q Q A L Q T G S 330  
331 \*

**Fig. 16**



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scFv(CEA6)

S Q V Q L L N G A  
GATCCAGGTTCACTG - - - CTGAATGGGGCCTA

M G S H H H H H G S I Q G R S P G T E P T A L Q T G S \*  
CATATGGGATCGCATCACCATCACCACGATCAGGATCAATCCAGGGAAGATCTCTGGTACCGAGGCCACCAACC--GCCCTGCAGACGGGATCCTAAAGCTTGAATTC  
Bam HI/Bcl I Bgl II Kpn II Bam HI Hind III

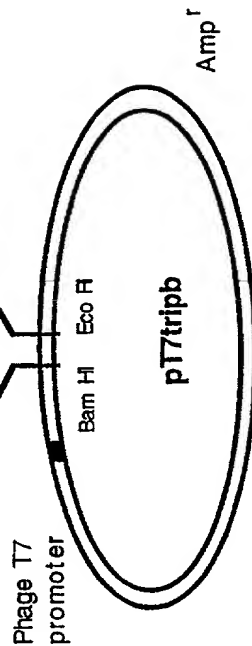


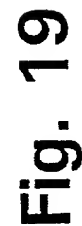
Fig. 17

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**H6FXtripb-scFv(CEA6) fusion protein**

1 M G S H H H H H H G S I Q G R S P G T E P P T Q K P K K I V 30  
31 N A K K D V V N T K M F E E L K S R L D T L A Q E V A L L K 60  
61 E Q Q A L Q T G S Q V Q L Q Q S G A E V K K P G S S V K V S 90  
91 C K A S G G T F S N S P I N W L R Q A P G Q G L E W M G S I 120  
121 I P S F G T A N Y A Q K F Q G R L T I T A D E S T S T A Y M 150  
151 E L S S L R S E D T A V Y Y C A G R S H N Y E L Y Y Y Y M D 180  
181 V W G Q G T M V T V S S G G G G S G G G G S G G G G S D I Q 210  
211 M T Q S P S T L S A S I G D R V T I T C R A S E G I Y H W L 240  
241 A W Y Q Q K P G K A P K L L I Y K A S S L A S G A P S R F S 270  
271 G S G S G T D F T L T I S S L Q P D D F A T Y Y C Q Q Y S N 300  
301 Y P L T F G G G T K L E I K R A A A E Q K L I S E E D L N G 330  
331 A \*

**Fig. 18**



**Fig. 19**

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**H6FXscFv(CEA6)-trpb-scFv(CEA6) fusion protein**

1 M G S H H H H H G S I Q G R S Q V Q L Q Q S G A E V K K P 30  
31 G S S V K V S C K A S G G T F S N S P I N W L R Q A P G Q G 60  
61 L E W M G S I I P S F G T A N Y A Q K F Q G R L T I T A D E 90  
91 S T S T A Y M E L S S L R S E D T A V Y Y C A G R S H N Y E 120  
121 L Y Y Y Y M D V W G Q G T M V T V S S G G G G S G G G G S G 150  
151 G G G S D I Q M T Q S P S T L S A S I G D R V T I T C R A S 180  
181 E G I Y H W L A W Y Q Q K P G K A P K L L I Y K A S S L A S 210  
211 G A P S R F S G S G S G T D F T L T I S S L Q P D D F A T Y 240  
241 Y C Q Q Y S N Y P L T F G G G T K L E I K R A A A E Q K L I 270  
271 S E E D L N G A G T E P P T Q K P K K I V N A K K D V V N T 300  
301 K M F E E L K S R L D T L A Q E V A L L K E Q Q A L Q T G S 330  
331 Q V Q L Q Q S G A E V K K P G S S V K V S C K A S G G T F S 360  
361 N S P I N W L R Q A P G Q G L E W M G S I I P S F G T A N Y 390  
391 A Q K F Q G R L T I T A D E S T S T A Y M E L S S L R S E D 420  
421 T A V Y Y C A G R S H N Y E L Y Y Y Y M D V W G Q G T M V T 450  
451 V S S G G G G S G G G G S G G G G S D I Q M T Q S P S T L S 480  
481 A S I G D R V T I T C R A S E G I Y H W L A W Y Q Q K P G K 510  
511 A P K L L I Y K A S S L A S G A P S R F S G S G S G T D F T 540  
541 L T I S S L Q P D D F A T Y Y C Q Q Y S N Y P L T F G G G T 570  
571 K L E I K R A A A E Q K L I S E E D L N G A \* 592

**Fig. 20**

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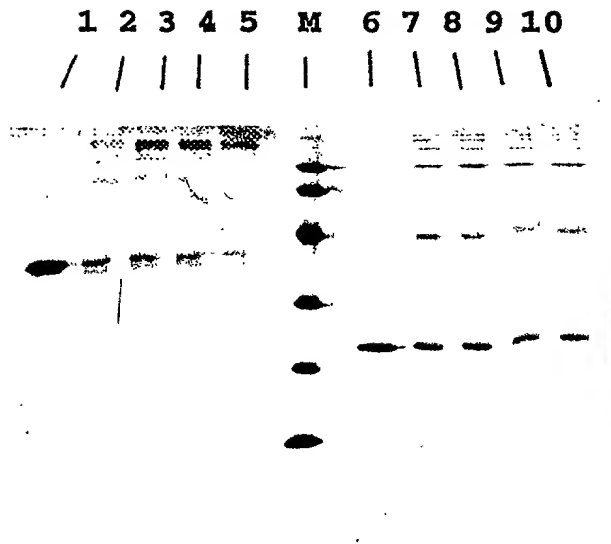


Fig. 21

**Combined Declaration for Patent Application and Power of Attorney**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name; and that I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

TRIMERISING MODULE

\_\_\_\_\_ the specification of which (check one)

[ ] is attached hereto;

[ ] was filed in the United States under 35 U.S.C. §111 on \_\_\_\_\_, as  
USSN \_\_\_\_\_\*; or

[ X ] was/will be filed in the U.S. under 35 U.S.C. §371 by entry into the U.S. national stage of  
an international (PCT) application PCT/DK98/00245; filed 11 June 1998,  
entry requested on 13 December 99\*; national stage application received  
USSN \_\_\_\_\_\*; §371/§102(e) date \_\_\_\_\_\* (\*if known),

and was amended on \_\_\_\_\_ (if applicable).

*(include dates of amendments under PCT Art. 19 and 34 if PCT)*

I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above; and I acknowledge the duty to disclose to the Patent and Trademark Office (PTO) all information known by me to be material to patentability as defined in 37 C.F.R. § 1.56.

I hereby claim foreign priority benefits under 35 U.S.C. §§ 119, 365 of any prior foreign application(s) for patent or inventor's certificate, or prior PCT application(s) designating a country other than the U.S., listed below with the "Yes" box checked and have also identified below any such application having a filing date before that of the application on which priority is claimed:

|                |                |                        |                                     |                          |
|----------------|----------------|------------------------|-------------------------------------|--------------------------|
| <u>0685/97</u> | <u>Denmark</u> | <u>11 June 1997</u>    | <input checked="" type="checkbox"/> | <input type="checkbox"/> |
| (Number)       | (Country)      | (Day Month Year Filed) | YES                                 | NO                       |
| _____          | _____          | _____                  | <input type="checkbox"/>            | <input type="checkbox"/> |
| (Number)       | (Country)      | (Day Month Year Filed) | YES                                 | NO                       |

I hereby claim the benefit under 35 U.S.C. § 120 of any prior U.S. non-provisional Application(s) or prior PCT Application(s) designating the U.S. listed below, or under § 119(e) of any prior U.S. provisional applications listed below, and, insofar as the subject matter of each of the claims of this application is not disclosed in such U.S. or PCT application in the manner provided by the first paragraph of 35 U.S.C. §112, I acknowledge the duty to disclose to the PTO all information as defined in 37 C.F.R. §1.56(a) which occurred between the filing date of the prior application and the national filing date of this application:

|                          |                        |  |
|--------------------------|------------------------|--|
| _____                    | _____                  | _____                                  |
| (Application Serial No.) | (Day Month Year Filed) | (Status: patented, pending, abandoned) |
| _____                    | _____                  | _____                                  |
| (Application Serial No.) | (Day Month Year Filed) | (Status: patented, pending, abandoned) |
| _____                    | _____                  | _____                                  |
| (Application Serial No.) | (Day Month Year Filed) | (Status: patented, pending, abandoned) |

I hereby appoint the following attorneys, with full power of substitution, association, and revocation, to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith.

SHERIDAN NEIMARK, REG. NO. 20,520 - ROGER L. BROWDY, REG. NO. 25,618 - ANNE M. KORNBAU, REG. NO. 25,884  
NORMAN J. LATKER, REG. NO. 19,963 - IVER P. COOPER, REG. NO. 28,005 - ALLEN C. YUN, REG. NO. 37,971\*  
NICK S. BROMER, REG. NO. 33,478 - \* Patent Agent

ADDRESS ALL CORRESPONDENCE TO  
**BROWDY AND NEIMARK, P.L.L.C.**  
419 Seventh Street, N.W.  
Washington, D.C. 20004

DIRECT ALL TELEPHONE CALLS TO:  
**BROWDY AND NEIMARK**  
(202) 628-5197

The undersigned hereby authorizes the U.S. Attorneys or Agents named herein to accept and follow instructions from PLOUGMANN, VINGTOFT & PARTNERS as to any action to be taken in the U.S. Patent and Trademark Office regarding this application without direct communication between the U.S. Attorney or Agent and the undersigned. In the event of a change of the persons from whom instructions may be taken, the U.S. Attorneys or Agents named herein will be so notified by the undersigned.

Title: TRIMERISING MODULE

U.S. Application filed \_\_\_\_\_, Serial No. \_\_\_\_\_

PCT Application filed 11 June 1998, Serial No. PCT/DK98/00245

I hereby further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. §1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

|  |  |  |                   |
|--|--|--|-------------------|
| FULL NAME OF FIRST INVENTOR<br>Hans Christian THØGERSEN                |  | INVENTOR'S SIGNATURE<br><i>HCTH</i>                  | DATE<br>22/05/00  |
| RESIDENCE<br>Mundelstrup, Denmark DKX                                  |  | CITIZENSHIP<br>Danish                                |                   |
| POST OFFICE ADDRESS<br>Ristrupvej 41, DK-8381 Mundelstrup, Denmark     |  |  |                   |
| FULL NAME OF SECOND JOINT INVENTOR<br>Michael ETZERODT                 |  | INVENTOR'S SIGNATURE<br><i>Mbberodt</i>              | DATE<br>25/5-2000 |
| RESIDENCE<br>Hinnerup, Denmark DKX                                     |  | CITIZENSHIP<br>Danish                                |                   |
| POST OFFICE ADDRESS<br>Teglhøjen 18, DK-8382 Hinnerup, Denmark         |  |  |                   |
| FULL NAME OF THIRD JOINT INVENTOR<br>Thor Las HOLTET                   |  | INVENTOR'S SIGNATURE<br><i>Thor Las Holtet</i>       | DATE<br>26/5-2000 |
| RESIDENCE<br>Frederikssund, Denmark DKX                                |  | CITIZENSHIP<br>Danish                                |                   |
| POST OFFICE ADDRESS<br>Roskildevej 104, DK-3600 Frederikssund, Denmark |  |  |                   |
| FULL NAME OF FOURTH JOINT INVENTOR<br>Niels Jonas Heilskov GRAVERSEN   |  | INVENTOR'S SIGNATURE<br><i>Nielsen</i>               | DATE<br>27/5-00   |
| RESIDENCE<br>Århus, Denmark DKX  |  | CITIZENSHIP<br>Danish                                |                   |
| POST OFFICE ADDRESS<br>Brendstrupvej 58, DK-8200 Århus N, Denmark      |  |  |                   |
| FULL NAME OF FIFTH JOINT INVENTOR<br>Jette Sandholm KASTRUP            |  | INVENTOR'S SIGNATURE<br><i>Jette S. Kastrup</i>      | DATE<br>6/6-2000  |
| RESIDENCE<br>Allerød, Denmark DKX                                      |  | CITIZENSHIP<br>Danish                                |                   |
| POST OFFICE ADDRESS<br>Tokkekøbvej 6, DK-3450 Allerød, Denmark         |  |  |                   |
| FULL NAME OF SIXTH JOINT INVENTOR<br>Bettina Bryde NIELSEN             |  | INVENTOR'S SIGNATURE<br><i>Bettina Nielsen</i>       | DATE<br>6/6-2000  |
| RESIDENCE<br>Greve, Denmark DKX  |  | CITIZENSHIP<br>Danish                                |                   |
| POST OFFICE ADDRESS<br>Strøhusvej 76D, DK-2670 Greve, Denmark          |  |  |                   |
| FULL NAME OF SEVENTH JOINT INVENTOR<br>Ingrid Kjøller LARSEN           |  | INVENTOR'S SIGNATURE<br><i>Ingrid Kjøller Larsen</i> | DATE<br>5-6-00    |
| RESIDENCE<br>Charlottenlund, Denmark DKX                               |  | CITIZENSHIP<br>Danish                                |                   |
| POST OFFICE ADDRESS<br>Ingersvej 23, DK-2920 Charlottenlund, Denmark   |  |  |                   |